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197636; P97637;

15-701-1998 (REL. 36, CREATED)

15-701-1998 (REL. 36, LAST SEQUENCE UPDATE)

15-701-1998 (PEL. 36, LAST ANNOTATION UPDATE)

15-701-1998 (PEL. 36, LAST ANNOTATION UPDATE)

THTERLEWEN-19 PREFURSOF (ILL2) (INTERFEREN JAMMA INCUCENCY

(ISW NAMA INFOIDS FAITER) (INTERLEGETH-1 JAMMA, (IL 100AM)
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P70380;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
17-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTERLEMKIN-18 PRECURSOP (II-18) (INTERLEMENT JANMAN VIT. GAMMA)
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OKAMURA H , ISUTUT H , KOMATSU T , YUTSUI TANIMOTO TI, TOPICOE E , CKUEA I , NUKADJAKITA K , NAMBA M , TANABE F , KONISHI K NATURE 378:88-91(1995).
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ILL18 OR IGIF.
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EUTHERIA: RODENTIA.
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EMBE, 066244, 01561736; -.
MGD: MGI-107936; IGIE.
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NABE F., KONISHI K., FUKUDA S..
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15-JUL-1998 (REL. 36, LASI SEQUENCE UPDATE)
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
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SUBMITTED (JUL 1997) TO EMEL/GENEARK/DOBJ DATA BANKS.

-I- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPILERY
AND STIMULATES INTERFERON GAMMA PRODUCTION IN THEILDER TYP
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F16889,
G1-AUG-1992 :
G1-AUG-1992 :
G1-NGV-1995 :
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR: H10462: --
PROSITE: PSONIO45: LON_SEP: 1
HYDROLASE: SERINE PROTEASE: AID-BINDING
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ATP-DEPENDENT ESOTEASE LA (DO 3-4-21.53)
                                                                                                                                                                                                                                                                               01-AUG-1992 (PEI. 23, CHEAIEL)
01-AUG-1992 (PEI. 23, IAST REQUENCE UPDATE)
01-AUG-1992 (PEI. 23, LAST AUGURNOE UPDATE)
101-AUG-1992 (PEI. 23, CHEAIEL)
101-AUG
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                                                                                                                  EUKABYOTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VEGQNEAKTNSLECGEKGESAQTTETETTYGDEKELVVAKSAVLSEFENYLTINKKVPTD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RO GRAKSINALFEAMNOLKQILLVSQHEADLEEPIPEDLEGVGTIANIIQLLKLPEETVKVL
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CALALYTIC ACTIVITY HYDROLYSIS OF LAPGE PROTEINS SUCH AS GLORIN, CASELN AND CRAATURATED SERVIM ALROMIN, IN PRESENCE OF ATP
                                                                                                                  SCROFA (PIG).
AFYOTA METANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCNIT: HOMOTETRAMER (BY SIMILARITY)
SUBCRITCH OF CONTINUE OF CATTOR OF ASMIC.
SIMILARITY SECONS TO PEPTIFASE FAMILY S16; ALSO KNOWN AS
LON FAMILY OF AIP-DEPENDENT PROTEASES.
L: U22729; C1573440; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO MAD OR TO THE REPORT AND MARKET BY STREET, MAD BELANVOOR PLEYELIGHMES BAULLOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SEQTREITEMYFOSE-------VEGLAVTESVKDSKMSTLSCKNKIISEE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259-495-512(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SECTION OF STREET AND SECTION OF STREET SECTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred No
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                                                                                                                        VESTESSATA, TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
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         2ABA_YEAST
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Best Local Similarity
Matches 27; Conserv
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Q00362;
Q1-APF-1993 (REL. 2
01-QCT-1996 (REL. 2
01-NGY-1997 (FEL. 3
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GENE 129-795-299(1993).

THYMOLYTE PRODUCEL BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOLYTE PROLITERATION BY INDUCTING IL-2 RELEASE, B-CELL MATURATION A PROLIFERATION, & FIRROGENASI GROWTH FACTION ACTIVITY.

MATURATION A PROLIFERATION IN THE INFLAMMATORY PRECOUNCE PRING IT-1 PROTEING ARE INVOLVED IN THE INFLAMMATORY PRECOUNCE PRING IT-1 PROLIFE AS ENCOURAGE PROMISE. AND AND ACELLAGENASE FROM SYNOVIAL CELLS.

THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25. CREATED)
01-007-1996 (REL. 34. LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35. LAST ANNOTATION UPDATE
PROTEIN PHOSPHATASE PPZA REGULATORY SUBGNIT
CONTROL PROTEIN 55).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDIINE: 02017859.
HEALY A M., 701.NIEROWICZ S.
DEPAOLI-ROACH A A., DRINGLE
                                                                                                                                                   BRUSCHI C.V.;
YEAST 13:55-64(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDCSS OF YGL1900 OF G1345.
SACCHARLMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FÜNGI: ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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HUETHER M.J., LIN
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 FTEI--FURVETERALIFMWYISTSQAE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16. FAD DOWNER OF THE FORM STANDARD AND STANDARD THE FORM STANDARD STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
FUNCTION: PHOSPHAIASE ZA AFFECIS A VARIETY OF BIOLOGICAL PROCESSE. IN THE CELL SHOP AS TRANSCRIPTION, CELL CYCLE PROPERSION AND CELLULAH MECHHOSENESIS, AND PROVIDES AN UNITIAL IDENTIFICATION OF CHILICAL SHORTHATES FOR THIS PHOSPHATASE THE RESULT OVERCAPPING. MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT CVERCAPPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPCRETORY PROTEINS.
SIMILARITY: BELONGS TO THE IL-1 FAMILY.
L, M86725, G154668; -.
; JN0724, JN0724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SURUNIT: MONOMER.

THE SIMILARTIC AMONG THE II-1 PRECUPSOPS SUGGESTS THAT THE AMINE PRES PROTEINS SERVE SOME AS YET UNLEFINED FUNCTION.

THE LAYK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENTE SUBSECT THAT II-1 IS RELEASED BY DAMAGET CETTS OR IS SECRETED BY A MECHANISM DIFFERRUNG FROM THAT USED FOR OTHER
                                                                                                                                                                                                              NIN=5286C / Plice / F
LINE: 97197971.
NEVINA M / MITMA E
                                                                                                                                                                                                                                                                                                                                                                  CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKRVPGHNKMEFESSLYEGHFLACQKED 129
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; MACROPHAGE; MITOGEN; INFO
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257 1
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                                                                                                                                                                                                                                                                       FYISTE
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                                                                                                                                                                                                                                                                                                                                                           NIEROWICZ S., SIAPLETON
A. DPINGLE J.R.;
. 11:5767-5780(1991).
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                                                                                                                                                                                                           PERTANI I.,
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: 5930DFAB CRC22;
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FUNDING FEAR EXCECTED IN SEVERAL EXCRESS CORMS, ALL OF WHICH NAISE FEAR COMPLEX A CATALYTIC SUBUNIT ASSOCIATED WITH NAISE FEAR COMPLEX ASSOCIATED WITH A SUBUNIT AND THE CORE COMPLEX ASSOCIATES WITH A SUBONIT ADEAS OF THE HOLDSNAYME.

ASSOCIATED WITH A SUBOR SUBOR SUBUNIT (SUBUNIT B), WHICH NEEDS INSIDENT BOOFERTIES FOR THE HOLDSNAYME.

MICASOCIATION AND WITH SUBUR SPECIES PROSERVATASE ZA REGULATORY ASSOCIATION OF THE HOLDSNAYME.
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THEM. BO PHYOL RES. COMMON. 188:1273-1279(1992).
TAYLOV
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PS 1925, PRSS 2: 1.
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822.36.24.
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LINED THE WARREST BY NEW YORK AND THE TREET SHOPE
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: Bred, No. 14;
24: Mismutches 57;
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Provid No. 4,9;
C. Mismonimber 56;
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Best Local Similarity
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SEQUENCE FROM N.A.
MEDLINE: 89016591.
LEONE S.F. FLANGS G.M. LAWMAN.M., GR
NUCLEIC ACIDS RES. 16:9054-9054(1988).
[2]
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BUILT O'T, WHITE O., OLSEN G.T. THOU L., FILTSCHHOMN R.D., GIVEN G.T., THOU L., FILTSCHHOMN R.D., DEVILED G. T., THOU L., CLOYELN F.A., JONGBERLE R. RETENDER R. RETEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1998 (FEI 10, CFEALE)
01-MAR-1989 (FEI 10, LAST SEQUENCE UPDATE)
01-NOV-1995 (PEI 32, LAST ANNOTATION UPDATE)
INTERTEURIN-1 PETA PERTUPSOR (II.-1 BETA).
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NMBL: U67525; G1499632; -.
TIGE: MJ0809; -.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
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EUKARYOTA: METAZOA: CHOSSATA: VERTERRATA: TETRAI DA: MAMMALIA.
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SEQUENCE 167 AA; [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                         CRAY P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
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Best Land &
Matches 30
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N A
KEDILINE: 85661582
LOMEDICO: P.T., GURIER II
LOMEDICO: P.T., GULLIER K
PAN Y-CLE., COLLIER K
NATURE 312-458-452(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-300-1986 (REL 01
01 001-1986 (REL 04
NTERFERKIN-1 ALEHA F
                                                                                             J. BIOL
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P01582:
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                                                                                                                                                          PHISPHORELATION AT SER-90.
MEDLINE: 88153709.
PHISCHER H II NICKELLS M
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MALISZEWSKI C F . BAKEF E.
GILLIS S., CERRETTI D.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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-! SIMILARITY: BELONGS TO THE IL-1 FAMILY.

BMBL: M35589; G163203; ..

EMBL: X12498; G449: -.

PMR: M37211: G163201: -.

PMR: M37211: M37201: INTEPLEUKIN_1; 1.
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SCHER H. IN NICKELLS M.W. CONTEN H.P.;

BIOL. CHEM. 563.4028.4028(1982);

FUNCTION: PROGUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

THYMOCYTE PROGUEED BY ACTIVATED MACROPHAGES, B-CELL

MAIURALION & PROGUEERATION, & FIRROPHAST GROWTH FACTOR ACTIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER.

THE SIMILARITY AMONO THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

THE LACK OF A SECTIFIC PYCHOLOGIC SEGMENT IN THE PRECURSOR SEQUENCE STRATEGY IS PELEASED BY DAVAGED CELLS OF IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNCI. 25:429-437(1988)
FUNCTION PROGRACED BY ACTIVATED MACESOPHAGES, IL-1 STIMULATES TRANSCOVER PROGRACED BY ACTIVATED MACESOPHAGES, IL-1 STIMULATES THE PROLIFERATION BY INDICING IL-2 PELEASE, B-CELL MALIURATION & PROLIFERATION & FIBORBAST SECURT FACTOR ACTIVITY IL-1 PROLIFIES ASE INVOLVEU IN THE INFLAMMATORY RESPONSE, BEING TORNITETED AS ENDOGROUS PROPRICED, AND ARE PROPRED TO STIMULATE THE RELEASE OF PROGRAMMANIAN AND COLLAGENASE FROM SYNOVIAL CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEKH -- NMEKKEVEYKIEI -- KNIVEFESVLYFNWYISTSGIEERPVFLGHFRAGQDITD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PENIDDIQSDLIFFQKRVPGHNKMEFESSLYE-------GHFLACQKEDD 130
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O1 (AST SEQUENCE UPDATE)
34. LAST ANNOTATION UPDATE)
HA PRECURSOR (ID-1 ALPHA)
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19. Mismatches 33;
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15F27850 0F632.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 266;
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            ACTIVITY
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Best Local &
Matches 31
                                                                                                                                                                                                                  ENTIAN K -D. KOFTTER D. POSE M. RECKER J. GPRY M. 11.2., MIEGEMANN E., SCHENK-GROENKINGER R., SERVOS J., WEHNER E., MOTTER B., GFR K., DIESTERHUS GRUENKEIN R., HELGES E., KIESAU P., KOROL S., KREMS B., FROET STEGERS K., RAUR A., BOLES E., MIOSGA T., SCHAARF-GERSTENSCHLANGER I., ZIMMERMANN F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-07-1994 (FEL 30 CREATED)
01-07-1994 (FEL 80 LAST SEQUENCE OPDATE)
01-NOV-1997 (FEL 35 LAST ANNOTATION UPDATE)
HYPOCHETICAL 70.2 K (FICELH IN EFET-COVER (NIERILM & REGION YHP)550 OP YER1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
_YEAST
                                                                                                                                                                                                                                                                                             STRAIN SCIBEC FORTIER D.
ENTIAN K -D FORTIER D.
NIEGEMANN E., SCHENK-GRO
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PPOSITE: PSO9253; INTERLEUKIN_1; 1.
CYTOKINE: MACEOPHANE: MITOGEN: INFLAMMATORY FESTONST; PYROCEN;
                                                 2 IMMERMANN F.K.;
                                                                      MEDITNE: 93255907.
                                                                                                                       STRAIN-S288C
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                             SUBMITTED (Arm: 1444) TO EMBL/GENBANK/DOBT DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SACCHAROMYCES CEREVISIAE (BAKER'S YEASI).
EUKARYOTA: FUNGI: ASCOMYCUTINA: HEMIASCOMYCETES
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0:289-203(1993).
236025; 0535468;
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NOV OF SET 16, TAKE SHOURDE UPDATE)
NOV OF SET 42, LAST ANNOTATION UPDATE)
NEERLE SIN S ATHRA PREPRIES (ISS) ALPHA).
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THE LANK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRETURSOR
REQUESTS SHAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
SHOTRE BUT HAY A MECHANISM DIFFERING FROM HALL USED FOR OTHER
SECURE BY PROTEINS.
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FUNCTON STATEMENT AND ACTIVATED MACROPHAGES, IL-1 STIMULATES
FUNCTON STATEMENT HY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYM STATEMENT HY ACTIVATED MACROPHAGES, B-CELL
MATUCAS ARE LINCALVED IN THE INFLAMMATORY RESPONSE, BEING
IL-1 STIENS ARE INVOLVED IN THE INFLAMMATORY RESPONSE BEING
IDENTIFIED AND ENDOTENDING SYROGEN. AND ARE REPORTED TO STIMULATE
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                                                                                                        GEN. INFLAMMATURY RESPONSE, PYPOGEN
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                                INTERLEUKIN-1 ALPHA
F-TENTIAL.
F-TENTIAL.
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Print No. 10
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· I (IN REF. 2).
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                                                                                                                                                                                                                                        Query Match 9.5%; Score 77.5; DB 1: Lenath 439;
Best Local Similarity 23.7%; Pred. No. 7.3;
Matthew 37, Conservation 26, Mismatches 46; Indois 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 BULT C T , WHITE O. OLSEN G J. ZHOU L., FLEISCHMANN K.D.,
SUTTON G.G., RIAKE J A , FITZGERALD I M. CLAYTON F.A. GODAYNE J.N.
KERLAVAGE A.B., DOUGHERTY B.A., TOMB J.-F., AGAMS M.D., REICH C.I.
OVERBEEK F., KIPKNESS E F., WEINSTOK K.G., MERKICK J.M., CLONEK A.
SCOTT J.L. GEOGHASEN N.S.M., WEILMANN J.F., PHEMANN J.M., CHONEK A.
OUTEBBRACK I.E., KELLEY J.M., PETERSON J.D., SAIOM P.W., HANNA M.C.,
OUTTON M.D., POSETTS K.M., HUPST M.A. KAINE H.P., BOPODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.B., VENTER J.C.,
SCIENCE 273.1058-1073(1996).

--- SIMILABITY TO M. JANNASCHIL MJOOFT AND SOME, TO ELOCAL YIEM.
EMEL. 1977.5: 3143434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q58221;
01-NOV-1997 (PEL. 35, CPEATED)
01-NOV-1997 (REL. 35, LAST SEOT
15-JUL-1998 (PEL. 36, LAST ANN-
HYPOTHFTICAL PROTEIN MJ0811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE, 96337999.
BULT C T , WHITE
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                                        11% FE-----SSLYEG-------HFLACQKEDDAFK 133
332 FEETIELASLYFGGGINFIMPLNRAMSLIKEHETFK 367
                                                                                297 DREIWCKAVALSI----TEIAMBENBDIYYIAFD......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 VILEISHIEL FVSAQNEDFPVILKELPHIERTIKDETSILLEFWEF
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                                                                                                                    53 DSEVBGLAVILSVKDSKMSILSCKNKIISFEEMDPPENIDDIGSDLIFFGKEVFGHNKME 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VILSVKDSKMSTISCKNK---IISEPEMDEPENDDDDDS (11+0)KVVPGHNKME-FESS 110
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                                                                                                                                                  BURNELANI SUSULALI BASADA BERTUTA - - - FUTANKI EKANDALI I
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∠7∪ AA:
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                                                                                  DGVBERKI NEKTII
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HTPG_HELPY

HIPG_HELPY P56116:

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RESULT

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Search completed: Time 22, 1999, 10.59.48 Job time: 74 sec
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VENIER J.C.;

VENIER J.C.;

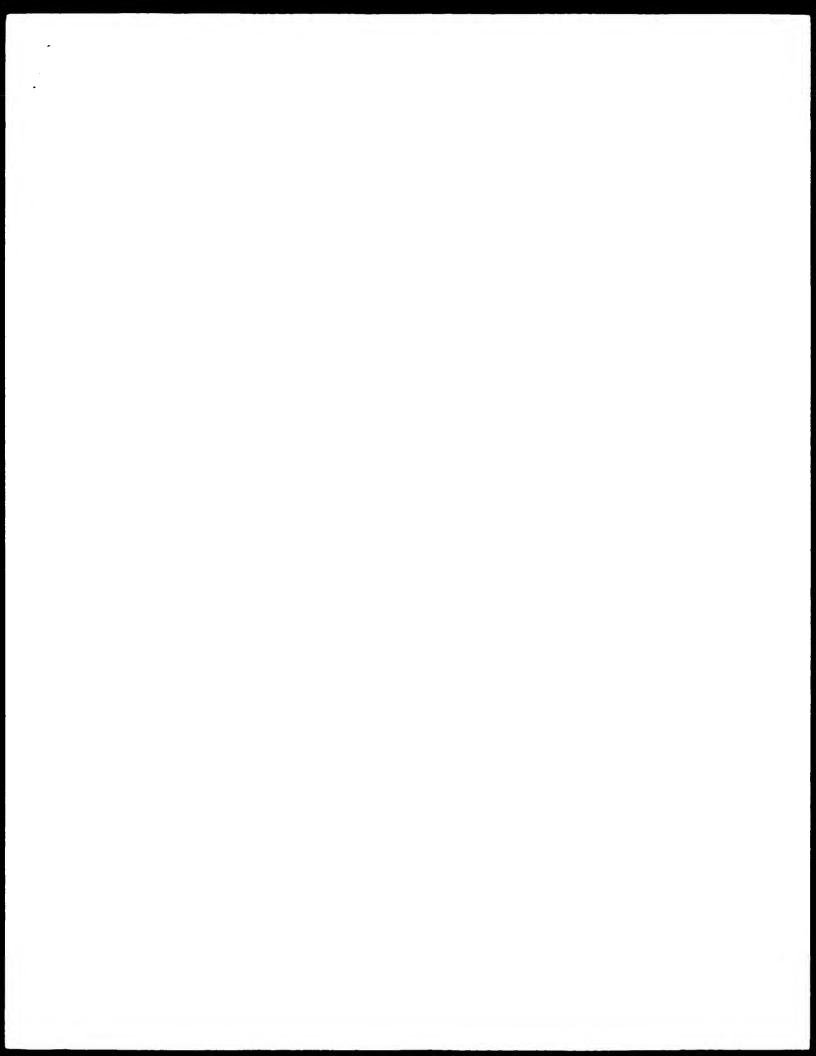
NATURE 388:539-547(1997).

NATURE 388:59-547(1997).

(BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

EMBL; AECCOS41: G2313300; -.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANOTATION UPDATE)
HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
HTPG OR HP0210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HELICOPACTER PYLORI (CAMPYLOBACIEK PYLORI).
PROMAPYGIA: GEACILLOUIES: SCOTOBACTERIA;
AFRORYC, MOTILE, HELICAL AND/OR VIBRIGID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00298; HSP90: 1.
CHAPERONE: AIP-BINDING: HEAT SHOCK.
SEQUENCE 621 AA, 71274 MM, 234A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 97394467.
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                                                                                                                                                                                           144 NSDQA 148
                                                                                                                                                                                                                                                             142 NGDKS 146
                                                                                                                                                                                                                                                                                                                                    6) EHIGTIAKSGTKNEISALSGDKKKDSALIGDEGVGEYSAEMVAS------KIVVQTKKV 143
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                                                                                                                                                                                                                                                                                                                                                                                                              ENIDD: -2SDLIFFQKRVPGHNKM-----EFESSLYEGHFLACQKEDDAFKLILKKKDE 141
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08-09-030-061-1
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STRAIR-BRIGHTON:
MEDILINE: 94233741.
MEYER H. OSTERNIEDER N., CZERNY C.P.;
"Identification of binding sites for neutralizing memoricual antibodies on the 14 kba fusion protein of orthopox virusos.
VIROLOGY 200:778-783(1994).
EMBL: X75158; G404264 - .
SEQUENCE 110 AA. 12514 MW: 41830309 CRC32;
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MEYER H., OSTERRIEDER N., CZERNY C.P.;

MIGENETIFICATION OF BIDDING SILES for neutralling accordingly and the following siles for neutral line according to the following siles of the fusion protein of orthogon viruses.": VIROLOGY 200:778-783(1994).

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VIRUSES: DSDNA VIRUSES.
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01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
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REPLIANCE FROM N.A.

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PA STITON G.G. SLARE J.A. FINESPALE L.M. CANANS M.D., REICH G.I.,

PA STITON G.G. SLARE J.A. FOR J.T., ANAMS M.D., REICH G.I.,

PA OVERBEER F., MIFKNESS M.F., WEINTON K.G. MERLTY T. OLOGOWAN.

PA STOTI J. GROWHARTH N.S. M. WEINTON K.G. MERLTY T. NGUYEN D.,

PA STOTION M.D., FORSER G.M., HUPSI M.A., KALNE B.P., BUPYLEVSKY M.G.,

PA CUTTON M.D., FORSER G.M., SMITH H.O., WOESE G.P., VENTER J.G.,

PA KLENK H.-P. FRASER G.M., SMITH H.O., WOESE G.P., VENTER J.G.,

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PROMITE, PROQUES; Adap_Comp_sub; 1.
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EUKARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
PIERYGOTA; DIPTEPA: BPACHYCEYA: MUSCOMOPPHA: EPHYDROIDEA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27: DR 3: Pred. No. 25; l: Mismatches
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Tred. No. 68;
1; Mismatches 0
                                                                                                                                               P. T.
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Score 27: DB Pred. No. 84; 0; Mismatches

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ALL T.
THE SOPHICA MELAN SIASTER (FRO
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ETHAYGES SET THAL BRATHET
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A MELAN A, AKTIKOPODA, TRACHFATA, HEXADODA, INS
A MELAN A, KANTIK TERA, MISTIMARERA, EFRYDROTIFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          × ^ ..
                          METAZ A. AKTHROTOPA: TRATOBATA: HEXARODA: INSECTA: LISTI STEERA: SPETNOTOAE: SPETNOTOAE: SPETNOTOAE: MANDUCA
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PRESSUREL OF CAST ANNOTATION UPDATE)
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AN ARTHRET III TRANHLATA, HEXARDEA, INSECTA,
RITHAR SHHENETODRAL SPHINGTOAR: SPHINGTNAR; MANDUCA
                                                                                                                                                 PATTO HAWKMOTH) (TOBACTO BORNWORM)
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TAT ADAPT F.M. 2: 1.
TAT ADAPT F.M. 2ABTT12D CRC12:
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                                                                                                   AKTHKOTOTA; [KACHEATA; HEXAPODA; INSECIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #2.14: Shore 27: DB 4: Length 54: #1:04: No. 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMPT AT A BOAR OF BY LATA BANK
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OIL (AST SPUGENCE HUDATE)
OF. LAST AND TATEM UPDATE)
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Pred. No. 91;
1: Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.1%: Score 27; DB Matches 5. Conservative 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 87.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
017901 PRELIMINARY) PRT: 1763 AA.
017901; 020887;
01-NoV-1996 (IREMELREL 01. CREATED)
01-NoV-1998 (TREMELREL 08, LASI SBOUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94150718.

WILSON S. AINSCOUGH F., ANDERSON K., BAYRNS D., BERKE M., BONFIELL MILSON S. AINSCOUGH F., ANDERSON K., BAYRNS D., GORDEL M., CONNER M., CANDELER M., CATRELLE P., LIGHTING J., LIAVO C., MCMITRAY A., MORTIMORE B., CICALLAGHAN M., PARSONS J., PERCY C., MCMITRAY A., MORTIMORE B., CICALLAGHAN M., PARSONS J., PERCY C., SONNHAMMER B., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., SONNHAMMER B., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., WALLKINSON-SPOAT J., WOHLDMAN P., WALSON A., WELNSTON R., WALKINSON-SPOAT J., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 368:32-38(1994).
EMBL: 789315; B315237; -.
PPAM: PEON928; Adapt comp_sub: 1.
SEGMENTE 425 AA: 48842 MN: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "2.2 Mb of Good grows burshed ide sequence from chromosome III of C elegans.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKAPYOTA: METAZOA; NEMATODA: SPCEPNENTEA: EHABDITIA: EHABDITIDA:
EHABDITINA, EHABDITOIDHA, EHABDITIDAE, PELODEKINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TREMBLREL, 04, CREATED)
01-JUL-1997 (TREMBLREL, 04, LAST SEQUENCE UPDAID)
01-JUL-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
K11D2.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family of alternate exone emonding the reactive site loop." J. BICC. CHEM. 271:28017 28027(1996). BMBL: U58361: G1378131: -. PEAM: PEU0079: Serpin: 1. PEU0079: Serpin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      002282;
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MEDLINE; 97067009.
JIANG H., WANG Y., HUANG Y., MULNIX A.B., KADEL J., JOLE K.
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"Organization of serpin general from Manduca secta. Evolution
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Mismatches

DB 3; i-math :25;

LEGRIAGE CRC3C;

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Search completed. June 22, 1999, 11:01:19 Job time: 165 sec
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Best Local :
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MEDLINE; 94:50718

WILSON R. AINSCOUGH P. ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,

WILSON R. AINSCOUGH P. ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,

BURTON T. CONNELL M., CORSEY F., COULSON A., CRAXTON M.,

DEAR S. OT Z. DIFFIN P., FAVELLO A., FULTON L., GARDNEP A., GREEN P.,

HAMKTINS T. HILLIER I., JUEN M., JOHNSTON L., JONES M., KERSHAW J.,

KIPSTEN T. I ALISTEP N., LATREILLE P., LIGHTNING J., LLOYD C.,

KIPSTEN T. I ALISTEP N., TATREILLE P., LIGHTNING J., ERPCY C.,

MUMUPRAY A. MOPTIMORE B., O'CALLAGHAN M., PARSONS J., PEPCY C.,

MINUPRAY A., SAUNCEPS D., SHOWNKEEN R., SMALDON N., SMITH A.,

SONNHAMMER E., TADEN P., SULSTON J., THIERPY-MIEG J., THOMAS K.,

VANDON M., VANGHAN K., MATEPSTON R., WATSON A., WEINSTOCK L.,

WILKINSON-SPECAT J., WOHLDMAN P.,

WILKING J.,

WOHLDMAN 
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MATURE 368:32-38(1994).

BMBL: 259852: E1321758: -.

EMBL: 259852: E1321758; JOINED.

BMBL: 259852: E1321758; JOINED.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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5; Conserv
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83.3%; Fred. No. 4.1e·02;
tive 1; Mismatches 0; Indels
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Bost Local Similarity 100.
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TISSUE-LIVER:
MEDLINE, ACUCALOS.
OKAMURA H., TSUTUL H
TANIMOTO T., TORIDIE
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P70380,
P70380,
15-701-1998 (PEL 36, LASI SECUENCE UPDATE)
15-701-1998 (REL 36, LASI SECUENCE UPDATE)
15-701-1998 (REL 36, LASI ANNUTATION UTDATE)
17-701-1298 (REL 36, LASI ANNUTATION UTDATE)
17-101-1298 (REL 36, LASI ANNUTATION UTDATE, LINCOLNY LACIDA, 
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Q14116;
Q14116;
15-JUL-1998 (REL 35, GREATED)
15-JUL-1998 (REL 35, GREATED)
15-JUL-1998 (REL 36, LASI SEMBLANE HPLATE)
15-JUL-1998 (REL 36, LASI ANNO UDDATE)
11-1998 (REL 36, LASI ANNO REFERENCEMMA IN SCHIG FACTURE)
INTERLEMENTAL PRECIPEOP (LL-19) (INTERLEMENTAL IN SCHIG FACTURE)
(IFN-GAMMA-INCUCING FACTURE) (LNIERLEUKIN-I GAMMA) (IL-1 GAMMA).

IL18 OR IGIF
HOMO SAPIENS (HUMAN).
EUTRAFYICA, MEIACHA, TH.FIAIA, VEHIESBAIA, ILIBALLA, FAMMALLA;
EUTHERIA: PRIMATES.
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ILSSUE-PERFITEEAL BLOUD;
CONTI B. KIM S.J. IN IMMC, DERWARK, TERT EATA BANKS.

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AND STEMPLATES INTERFEED GAMMA FRICTIEN IN THE STEELS CELLS
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MEDLINE; 95247646.

USHIO S. MAMBA M., OKUPA T., HATTOFI F.,

TANABE F., ECNISHI F., MICALLEF M., FUJII
EUKUDA S., IKEDA M., OKAMUPA H., KURIMOTO
J., IMMUNCL. 156:4274 4279(1996).
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SEQUENCE FROM N.A.
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EUKARYOTA, METACCA CHIEDAIA.
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M.: TORISCE K., TAMIMOTO
M.:
                                                                                                                                                                                                                                                                                                                                          TETEAFIIA, MAMMALIA
          HATTOPI
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(6, LAST SEQUENCE UPDATE)

(6, LAST ANNOTATION OPDATE)

(8 (LAST ANNOTATION OPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.4.
Mismatches
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Best Local Similarity
Totobes 5; Conserve
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                                                                                                           YOGE_HAEIN
                                                                                                                                                         RESULT
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Best Local
P43980;
01-NOV-1995 (REL. 32, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ADRIA 85L030:
MEDLINE, 94288641.
PINCE A . DUFEUP A . TE POSAM S . HHEAULI D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-1994 (BET. 30, CREATED)
01-00T-1994 (BET. 30, LASI SEQUENCE OPDATE)
01-NOV-1995 (REL. 30, LASI SEQUENCE OPDATE)
101-NOV-1995 (REL. 32, LASI ANNOTATION UPDATE)
LACITICIN 481, DACINGOGCIN BIOSYNIHESIS PROJECT ONNUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-10 INAM (FIT W. LAST SELIENT INSATE)
15-JUL-1998 (REL RG. LAST ANNOTATION QUARTE)
INTERLEUKIN-18 PRECURSOR (IL-18) (INTEREERON-GAMMA INDUCING FAUTOF)
(IFN-GAMMA-HUDGING FACTOR) (INTERLEUKIN 1 GAMMA) (IL-1 GAMMA).
IL18 OR IGIF.
                                                                        YOGE_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEVERNEE
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EURAARYOTA, METAZCA, CHCEDATA, VEHIEBBATA, IBIBNIISSI, MAMMANITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPI..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HACTOCOCCUS LACTIS (SUBSET LACTIS) (SIREFFOCUCTOS LACTIS).
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                                                                                                                                                                                                                                                             569 NDQILF 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL ENVIRON. MICROBIOL. 60:1652-1657(1994).
FUNCTION: COULD BE IMPLICATED IN THE PROCESSING OF THE LANTIEL FITC LACTICIN 481/LATIONSCIENTLE U04057: G433322: -.
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121
194 AA;
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Pred. No.
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INTERLEUKIN-18.
MISSING (IN ISOFORM ALPHA).
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Pred. No. 1.7;
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                                                                                186
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01-001-1996 ()
HYPOTHETICAL ()
HI0304.
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                                                                                                                                                                                                               MOYLE
3130M
                                                                                                                                                                                                                                                                                                                                 P26012,
01-MAY-1992 (REL. 22, CREALED)
01-MAY-1992 (REL. 22, LAST SECUENCE UPDATE)
01-MMY-1994 (REL 24, LAST ANNOTATION HEDATE)
INTEGRIN BETA-8 SUBMNIT PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                     LHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN. SEQUENCE 186 AA; 2
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-1- SIMILARITY: STRONG, TO E.COLI
EMPL: 022716; 01572273; -.
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                        EUTHERIA: PRIMATES
                                                                                                                                                                                                                                                                                                              HOMO SAPIFUS (HIMAN)
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LE M., MAPIER M.A., MCLEAN J.W.,

LE M., MAPIER M.A., MCLEAN J.W.,

FUNCTION, 255:13450-13459(1991).

FUNCTION AS RECEPTAS FOR SELL AGRESION MSLECULES.

FONCTION AS RECEPTAS FOR SELL AGRESION MSLECULES.

STRENGT DIVERS OF AN AIPHA AND PETA STRUNKT RETA-8 ASSOCIATES
                                                                                        SIMILARITY: BELÖNGS ID THE
                                                                                                                                        WITH ALDEA-V.
STROTTLINGAR LOCATION TYPE I MEMBEANE PROTEIN STROTTLINGAR LOCATION OFFICE TRANSFERRING REPORTS.
                                                                                                                                   EMBRYONIC KIDNEY CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MT TYTE
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                                                                                                                       THE CYSTEINE RESIDUES ARE
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34. LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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INAMINE J.M., LOECHEL S
GENE 92:250:267(1989).
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MKGPC_MYCKE STANDAPE: PPI: 1052

FL2747, 144481, 143481, 144424, 144385, 2

01-AUG-1991 (REL. 19, CREATED)

01-AUG-1991 (REL. 19, LASI SEQUENCE UPDAT

01-NOV-1997 (REL. 35, LASI ANNOTATION UPD
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CARBURYL
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MEDLINE 92051396. G 37:
MEDLINE 92051396. ETTERSON S.H., SCHERARM H., HC F.-C., B. NCCLETC ACIDS KES. 19.6027-6031(1991). EMBL. M:1431 G150160: ".
EMBL. M:1431 G150160: ".
EMBL. B:1455. TJATP377 ...
EMBL. SCHERARM SG409890: ".
                                                                           MEDLINE: 94975230.
PETERSON S.N., HU P.-C., BUTT K.F
J. BACTERIOL. 175:7918-7930(1993)
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PENKAPYSTA, TENEFISSES:
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01:FEB-1991 (REL 17, C 01:FEB-1991 (PEL 17, L 01:FEB-1994 (REL 28, L 4 KD FUSION PROTEIN. A27L.
MEDLINE: 88036210.

RODRIGUEZ J.F., ESTEBAN M.;

J. VIROL. 6:3550-3554(1987).

-!- FUNCTION: THIS PROTEIN APPEARS TO PLAY AN IMPOPTANT ROLE IN VIPTOPEMENTATION. THE LEVEL OF CELL FUSION. THE N-TERMINAL PROXIMAL REGION IS ESSENTIAL FOR FUSION ABILITY. ESSENTIAL IN PUSING THE OUTERWOST OF THE TWO GOLGI-DERIVED MEMBRANES ENVEL FINE THE VIPTOPEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P11258;
01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 21, LAST SEQUENCE UP
01-PER-1994 (REL. 28, LAST ANNOIATION
14 KD FUSION PROTEIN.
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VIRIDAE: DS-DNA ENVEL/GED V
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VIROLLOGY 179:517-553(1990).

-!- FUNCTION: THIS PROFEIN APPEARS TO PLAY AN IMPORTANT ROLE IN VIEW
FENETRALION AT THE LEVEL OF CELL FUSION. THE N-TERMINAL PROXIMAL
REGION IS ESSENTIAL FOR FUSION ABILLITY. ESSENTIAL IN FUSING THE
OUTERMOST OF THE TWO GOLGI-DEPIVED MEMBRANES ENVEL TING THE VIEW
WITH THE PLASMA MEMBRANE, AND IN ITS SUBSECTENT RELEASE
EXTRACELLULARLY.
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VISCLUDY 179.547 266(1990)
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VIRIDAE, DS:DNA ENVELOPED VIRUSES.
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MEDLINE; 91021027.
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_BIOL. CHEM. 266:13712-13718(1991).
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SUBCELLULAR LOCATION: ENVELOPE FRACTION OF VIPTOMS
SIMILARITY: TO OTHER POXVIBUSES FUSION PROTEIN.
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EMBL: M61197; G335A629: -.

EMBL: M51313; G335A629: -.

EMBL: M5731B: G50244; ..

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948455;
91-NOV-1997 (REL. 35, CREATED)
91-NOV-1997 (REL. 35, LASI SEQUENCE UPDATE)
91-NOV-1997 (REL. 35, LASI ANNOTATION OPERATE)
91-NOV-1997 (REL. 55, LASI ANNOTATION OPERATE)
NIPOTHERICAL 44 & KI PROTEIN IN TPS FEATURE)
KLEBSIELLA PREMMONIAE.
PROKABITIA 35ACTIONTES: SOUTHANTEETA: FACULTATI
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EMPL: DOIDT: GT47668.
HYPCTHETICAL PROTEIN.
SECTEMOR WAS AN 44576 MM. AIN
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                STRAIN-BRISTOL N2;
PAULEY A.;
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Prod No 18.
Mismatches
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EMBL: X17617; G55473; -.
EMBL: X17617; G55473; -.
EMBL: X17614; G202452; -.
EMBL: X176145; G202452; -.
EMBL: X17617; A37107.
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PIR: A37107
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FIESZD; O1-APP-1990 (PEL 14 CREATED)
O1-APP-1990 (PEL 14 LASI SEQUE
O1-OCT-1996 (PEL 14 LASI ANNU)
ZINC FINGER PROTEIN ZEP-35.
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EMBEL 002506) 0746579 -
WURMERN TWICHING CE02448
HYPOTHETICAL PROTEIN.
SEQUENTE 404 AA: 24062 N
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MUS MUSCULUS (MOUSE)
ENFASYNIA: METACCA:
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Obser-1996 (first entry)
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Interferon gamma, inducer, renyamma, immunocompetent cell: antiviral: antitumour; antiseptid, immunocompetent cell: antiviral: antitumour; antiseptid, immunoregulatory, platelet-increasing agent: therapy, procedulato, cadylama acuminatory; platelet-increasing agent: granuluma: mycosis fungolides; rhounatism; allergy; cytorixicity; AlDS: granuluma: mycosis fungolides; rhounatism; allergy; cytorixicity; AlDS: Aller Toell: interleuxice? Includent mercals fugure. TNF; adoptive immunotherapy, monoclonal antibody.

Synthetic.

EP-692536-A2.

17-JAN-1995; 304906.

14-JUL-1994; JP-194162.

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18-SEP-1995; JP 274988.
29-SEP-1995; JP 274988.
                                                                                                                                              A novel human protein (899558) induces interfer m-vamma (IFN-vamma) prodn. by immunocompetent orbits to pendances the cylosockery of killer cells and/or induces the formation of killer orbits (c.u. NK cells, lymphokine-antivating killer (IAK) orbit, and mythtwin Troplis). Recombinant IFN-vamma induced protein can be produced in high yields using host cells, esp. Escherichia cell, transformed with a vector carrying the encoding cDNA (T32402). It is useful as an antiviral antitumor, antibacterial, immunoregalatory and blood platelet enhancing adent, and can be used in adeptive immunorhorapy it is also used to raise monoclonal antibodies. A full length sequence is given in R99560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR amplification of the CRNA (see also TR2404-10) and expression in Escherichia coli XI-1 Blue MEPTEAN allowed product of invombination inducer protein. This was used to construct hyperagonal antipolity produced anti FEN-gamma inducer protein monoclonal antibody H-ImAL useful in the detection and purification of the inducer principles (see also R99558).
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 40; 48pp; English.
A novel human protein (R99558) i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
Fukuda S. Kobro K. Kunivata I. Ku
Taniquchi M. Tanimoto T. Toriqoo K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1996 (first entry)
Human mature interferon-damma inducer protein.
Interferon-damma inducer protein, IEN-damma, antivital, viruelder antitumeur, antibacterial; immunuregulatur, ad-etire immunotherapp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R99558 standard: Protein: 157 AA.
R99558;
29-SEP-1996 (first entry)
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N-PSDB: T32402.
                                                                                                                                                                                                                                                                                                                                                                                 disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding interferon-gamma prodm.-inducing polypeptide
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1 FEDMID 6
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                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 73
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                                                       100.0%; Score 33: DB 1: Length 157: 100.0%; Pred. No. 2.7:
                                         C
                                         Mismatches
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RESULT
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Best Local
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D2 WAY 1996.
30-WOV-1994. JP-38429.
15-NOV-1994. JP-384203.
D3-FEP-1994. JP-078924.
10-WARR-1995. JP-078937.
18-SEP-1995. JP-282062.
29-SEP-1995. JP-282062.
                                          Example A-2-2: Page 36-37, 18pp, English.
A dovel mouse protein (R99559) induces interferon-gamma (IFN-gamma) prodn by immunocompetent cells. Its sequence was deduced from that of a cUNA colone (13447) (solated from a mouse liver library becombinant IFN-damma induces protein can be produced in high yields using host wells sep Exchericable coll, transformed with a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding interferon gamma prodontinducing polypeptide to treat and prevent, e.g. viral disease, malignancies and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
Eukuda S. Kohno K. Kunikata T. Ku
Taniquohi M. Tanimutu T. Torigoo K
WPI; 96-2552877-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interferon gamma inducer protein. IFN-gamma, antiviral: viruelde, interferen-jumma inducer protein. IFN-gamma, antiviral: viruelde, antiviral: artiviral: viruelde,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carrying the cDNA. Sequence 157 AA.
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Interferen iaama indice: protein, IFM-gamma, activinal; virueide;
artituron: artitarrenial inducenegulator, adoptive immunotherapy;
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37. .]
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Kunikata T.
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  Kurimoto M,
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                                                                                         Query Match
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10-NOV-1995; 3P-304203.
15-NOV-1994; JP-304203.
23-FEB 1995; JP-028340.
10-MAR-1995; JP-028357.
18-SEP-1995; JP-028357.
29-SEP-1995; JP-028357.
20-SEP-1995; JP-028357.
20-SEP-19
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The mature portion of a novel bullar protein (64550); indexes interferon gamma (IEM-yaumma) product. by immunocompetent cells. I interferon gamma (IEM-yaumma) product of a cNA clone (732404) ebtd. from a numun liver likrary. The protein enhances the greatextity of Relice relis and/or induces the formation of Killer cells (e.g. NE cells, and/or induces the formation of Killer cells, and cytocoxic Toelis, lymphokkine-activating killer (LAK) cells, and cytocoxic Toelis, lymphokkine-activating killer (AEK) cells, and cytocoxic Toelis, antitumor, antibacterial, immunocepalating and blood platelet enhances are in 1981 to be used in adoptive immunocthorapy. It else used to raise menocolonal antibodies.
                                                                                                                                                                                                                                                      Example A:3.6; Page 17: 48pp; English.

Example A:3.6; Page 17: 48pp; English.

Fryptic peptides (R9956) and R99562; correspond to amino acids 79:10: 10.7 £140. Experitively, if a novel interferon gamma (ITN-quamma) inducer protein identified in mouse liver. The fertile acids and interferon per protein for mouse liver of that were utilized in the amplification of mouse liver cDNA, leading to the isolation of a clone (IT2403) coding for mouse IFN-gamma the isolation of a clone (IT2403) coding for mouse IFN-gamma.
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NA For did interfere gamma producted delegacity of the to these and prevent, e.g. wind disease, maildraneles and
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                                                                                                                                                                                                                induce: protein (R99559).
Sequence 18 AA;
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Sarity 100.0%;
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Numbers
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Fred. No. 0.26;
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cerl Sociatity 100.0%, Prod. No. 2.7
8 6 Occurrentivo O Mismatches
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36 - 04/74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating e.g. muliquant tumours, viral, bacterial or
                                               to the tester of many production is immunocompetent only a true to seed as the major component in a drug for the major component tumours, viral diseases
                                                                                                                                                                                                                                 Fig. (1): [2pp: Japanese.
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Limen immunerompetent cell: malignant tumour;

Leg : effectil infection: immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thus in protein for induction of interferon-gamma.
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W24258
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Best Local Similarity
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                                                                                                                                                                     10-JUL-1997. U20432.
20-DEC-1996: U20432.
29-DEC-1995: US-580667.
(INCY-) INCYIE PHARM INC.
Cocks BG. Coleman R. Hawkins PR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \frac{\kappa \omega_I}{\text{Misc\_difference 140}} Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W31757 standard: Protein: 193 AA. W31757; 15-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune diseases (Claim 1: Page 9: 12pp: Japanese. This sequence represents a protein which induces interferon-gamma production in immuney expetent defits. This protein may be used as the major component in a drug for the prevention and treatment of e.g. malianant tumours, wiral diseases, bacterial into tions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J09157180-A.
17-JUN-1997.
24-JAN-1996;
                                                                                            WPI; 97-363677/33.
N-PSDB; T74988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interferon gamma inducing factor-2 (ISIF-2) E140: variant.
Interferon gamma inducing factor 2, ISIF-2, Teachlyter lymphocyter huma
inflammation; proliferation; differentiation; maturation; fissue damnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A drug containing a polypeptide which induces interferent quamma useful for treating e.g. malignant tumours, viral, bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-1995; JP-2/9906
10-MAR-1995; JP-078357
29-SEP-1995; JP-2/1988
compounds to diagnose, freat or prevent tissue damage associated
                                      Novel interferon gamma inducing factor-2 - used to screen to:
                                                                                                                                                                                                                                                                                                                                                                                                                             W09724441-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Interferon-gamma; immunocompetent ocil; mailgnant tumour; viral disease; bacterial infection; immune disease.
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Sequence 157 AA:
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97-969391/74.
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100.0%;
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Pred. No. 2.
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2.7:
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PS Chaim is the protein sequence of interferon gamma inducing factor-2
CC (JOSP-2). An IOSP-2 variant (W2775) and an IOSF variant (W22049).
CC Which has been a literate transcript, also exist. Probes derived from the nucleic acid sequences can be used to guantify the expression of COSF-2 in conditions that are associated with inflammation or aberrant expression of IOSF-2. The protein can be used to screen for compounds that interfact with IOSF-2, such as antibodies, antagonists or other can interfact with IOSF-2 such as antisense sequences) of COSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of treat IOSF-2 (Maintip: The protein can also be used to diagnose, provent of the can also be used to diagnose and the can a
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CC This protein sequence represents an interferon gamma inducing factor-2 (IGIF-2) variant. Identified from a liver cDNA library. This sequence coldities from IGIF-2 identified from a I-lymphocyte cDNA library (Mid47), in that amino acid 140 is found to be changed from Arg to Ile. A second colditary, W27843, also exists. From the function acid colditary represents the representation of IGIF-2 in conditions that amino acid to year tip the expression of IGIF-2 in conditions that are associated with inflammation or abstract expression of IGIF-2.

The protein and moved to serve for compounds that interact with the protein and moved to serve for compounds that interact with the protein and in the sequences) of IGIF-2 expression or activity. The protein and its to sequences of IGIF-2 expression or activity. The protein also be used to diagnose, nevert or treat IGIF-2 induction of prohiferation of ifferentiation or maturation of leucocytes or compounds that interact with inflammation. differentiation or maturation of leucocytes or lymphocytes, reporting in relation to tissue damage associated with inflammation.

Components of the sequence of the sequence of the sequence of the province of the sequence of the sequence of the sequence of the Idia and the sequence of the sequence of the Idia and I
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W09724441-A1.
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Interferon gamma inducing factor-2 (IGIF-2) protein.
Interferon gamma inducing factor-2. IGF-2. husbayte. lyn
Inflammation: prolliferation: differentiation; maturation;
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14-JAW-1998
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1 FEDMID 6
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ide to diagnose, treat or prevent tissue damage associated
                                                                     $|milarity 100
6: Conservative
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Similarity 100.0%; Prod. No. 3.4;
6: Conservative 0: Mismatches o
                                                                                                      100.0%;
100.0%;
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                                                                                                      Score 33; DB 1;
Pred No 3 4;
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Critic private sequence represents a newel protein from monse liver cells.

Critic private sequence represents a newel protein from monse liver cells.

This private form quanta (IR garma) production in immunocompetent cells in the private sequence of the limit mour for antition of the first private (including antition) or antibacterial agent.

Critic formation: It is used as an antitionation agent for antitionour and in the treatment of atapic or immune system discourse; e.g. assimated and in the treatment of atapic or immune system discourse; e.g. assimated and in the free memorian. When formalisted with interleuktion it is also used to treat leukepaenia and thrombocytopaenia associated with radiotherapy or chamotherapy of leukapaenia and other cancers, when used to antition of the protein significantly improves the interleup of allower with the rediction (before sequence 157 AA).
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 26-SEP-1996;
20-SEP-1996;
26-SEP-1995;
                                                      Homo sapiens.
EF-767178-A1.
09-AFR-1997.
                                                                                                         L6-JAN-lyge (first entry) N-terminal fractment of interferon gamma inducer protein. Interferon gamma, INN-gamma, activiral, antichector radification of interferon gamma, INN-gamma, activiral, antichector of them. therapy, leak-by-arthrombocytopenta, inconsequent cell; asthma; hayfover rheumatism; interleukin; killer cell.
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26-SEP-1996; Jr-270725.
29-FEB-1996; JF-067434.
(HAVE) HAVASHIBADA SEIBUTSU KAGAKU.
AKITA K. BUJIL M. Kurimoto M. Nukada Y., Tanimoto T;
WPI; 97-205381/19.
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Interferen-gamma, IFN-gamma antiviral; antioncotic: radiotherapy:
Inmunoregalatory, intitumor agent, chamatherapy, leak-pagenia:
thromborytopagenia inmunor ampetent cell: asthma: bayroscr:
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Best Local Similarity 100.0%; Score 33; DB 1; Length 157;

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GenCore version 4.5
Copyright (a) 1993 - 1998 Compages Ltd

OM protein : protein search, using as model

Run on: June 12, 1993, 10:58:43 : Search time 61.51 Seconds (without alignments)
3.654 Million cell updates/sec

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1 02 *:onld: A(2002) Jennel: 1006 *:onld: bango 20. Mar:1000
1 02 *:onld: bango 20. Mar:1000
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                                                                                      "High "1861', High "Feel", Fill 450462, MITS.YERICQ:
"13 % Fils. Heddessey, F.M., 2ekl, 5., Kimp, "
"1 of a library, Fabruary 1994
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1: Mismatches
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Cell 60, 705-717, 1990
Cell 60, 705-717, 1990
A:Title: A putative ATP binding protein influences the fidefilty of brancapolic A:Reference number: A32720: M910.90182661
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AAP-binding protein PRP16 - yeast (Saccharomyces cerevisiae)

C.Species: Saccharomyces cerevisiae

C.Patc: 03-May-1994 *sequence_revision 03-May-1994 *fext_chapac (%-Jun-1996 C)Accession: S28164; $42015: A32720; $599127

B.Baladown, V. Ballesta, J.B.G. Bou G. del Rey, F.; Esteban, F.E.; Narc.1-Nuttale submitted to the Protein Sequence Database, March 1994
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A.Rosidler: 122; V.,224,77.026 754 .000.
A.Rosidler: EXECUNCYS EXEUNCY928 NID.;172334.
R.Gietz, R.D.: Prakash, S.
Gene 74, 535-541, 1988
                                                                                                                           A,Experimental source, strain $2880
S.Burjess, S., Couto, J.R.: Guthrie, C.
                                                                                                                                                                                                                           A:Molecule type: DNA
A,Residues: 1 1071 <GAR>
A;Cross-references: EMBL:227116;
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F:410-416/Fegion: basic
F:711-754/Region: acidic
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A;Crose-references: GP-M25050; NID:q172332; PID:q172333
C;Comment: This protein is one of the products of five agree essential than
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J. Bacteriol. 171, 1862-1869, 1989
A.Tille. Nucleofide sequence of the Wild-Lype RADA
A:Reference number: A32832, MUID:89197751
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A Tress : Pfriedre CMF:
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A:Residues: 1-754 <MUL>
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Pred. No. 77;
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C:Accession. 224
R:Alterachmig:
Eur. J. Biochem.
A:Title: Novel
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A:Molecule type: DNA
A:Mosjibes (1964-197 FMA-197) cpgs:
A:Cluss-teferences: GB:M31524; NID:g172259; ELD:g172270
C:Genetics:
Richard F. Righaus C. Mueller, H.P. Lindberg, M. Bur. J. Bicthom, 202, 1041-1048, 1931
A. Hiller W. Bicthom, 202, 1041-1048, 1931
A. Hiller W. Bicthom, 1040-1040
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C. Keywords: fibronectin binding
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0:Species: Staphylococcus aureus
0:Date: 13-7an-1995 #sequence_revision 13-7an-1995 #text_change 09-Sep-1997
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A:Accession: $24378
A:Status: translation not shown
A:Molorub: type: DNA
A:Residues: 1 270 (AMI)
A:Cross::sformance DMST MGF694 NID (458)
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O:Species: Pseudomonas sp.
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R:Joengson F : Sign
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Bost Inna Similarity Pa
Matches Si Corservative
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Rost Total Similarity 93,3%;
Matches 5. Conservative
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#3. (*) Fred. No. 45:
Mismatches
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A; Gene:

yloN

Dauperfamily: conserved hypothetical protein HI0365

C; Genetics:

A:Experimental source: strain 168

NID: 12637 (02)

A; Molecule type: DNA A; Residues: 1:363 < KUN>

A;Status: preliminary; nucleic acid sequence not shown; translation not slown

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Claccession: #69878

Claccession: #69878

R:Kunst. F. Ogasawara. N. Mcczer. I.: Albertini. A.M.: Alicuit. C. Alcerch. V.: Ber C.: Bron. S.: Brouillet, S.: Bruschi, C.V.: Caldwell. B.: Alphara, V.: Sirter N.M.: A.: Ehrlich, S.D.; Emmerson, P.T.: Entian, K.D.: Errinaton, J.: Fabrot, V.: Sirter N.M.: A.: Ehrlich, S.D.; Emmerson, P.T.: Entian, K.D.: Errinaton, J.: Fabrot, V.: Martine, V.: Sirter, V.: Lipy A.: Aluthors. Fritz, C., Fujita, M., Fujita, Y.; Fuma, S.: Galizzi, A.: Galizzi, A.: Galizzi, A. Galizzi, A.: Galizzi, A.: Galizzi, M. Roningstein G.: Krogh, S.: Kumane, M.: Kurita, K.: Lapidas, A.: Lardino, S.: Maree, M. Koningstein G.: Krogh, S.: Kumane, M.: Kurita, K.: Lapidas, A.: Lardino, S.: Jaube, A.: Unitaries, A.: Odiwara, A.: Oddega, B.: Park, S.H.: Parro, V.: Poll, T.M.: Porretteilus, M.: Schl. Authors: Schropeter, P.: Scoffone, F.: Sckliquehl, J.: Scklawska, A.: Scrut, S.: Schl. Authors: Schropeter, P.: Scoffone, F.: Sckliquehl, J.: Scklawska, A.: Scrut, S.: Vanden, K.: Martine, F.: Yoshikawa, H.: Danchin, A.
A:Title: The complete arename soquence of the Gram-Govilla; laterium Buctills, Schl. M.: Rocession: F58878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein ylon - Bacillus subtliss C:Species: Bacillus subtliss C:Species: Bacillus subtliss C:Date: 05-Dec-1997 #fext_cluste 14-Sep-1-+P
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A:Gene: aq_474

A:Gene: aq_474
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A:Accession: H70342
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A;Residues: 1-410 <AQE>
A;Cross-references: CR-AECOSS91; NID:g2982119; FID::L98:129; OB:AECONGS
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C:Species: Aquilex acclicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Sep-1998
C.Accession_ E70342
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Best Local Similarity 83.5%;
Matches 5; Conservative
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Pred. No. 1.1e+02;
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O; Mismatches
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RESULT 15
S64082
probable membrane protein TGL075c · yeast (Saccharomyces cerevisiae)
N.A.ternate names: hypotherical protein G3219
C:Species: Saccharomycus cerevisiae
C:Species: Saccharomycus cerevisiae
C:Date. 17:Maj 1666 #sequence_tevision 17 May-1996 #text_change 14-Nov-1997
C:Accession: S64062
R:Rieger, M.: Mueller-Auer, S.: Brueckner, M.: Schaefer, M.
submitted to the Frotest sequence Database, May 1996
A:Reference number: S64071
A:Reference number: S64071
A:Residues: 1:387 KRIES
A:Molecule type: DNA
A:Residues: 1:387 KRIES
A:Molecule type: DNA
A:Residues: 1:387 KRIES
A:Molecule type: DNA
A:Residues: 1:387 KRIES
C:Genetics: Schill Schile Still S288C
C:Genetics: transmembrane protein
C:Reywords: transmembrane protein
E:311-277.7:mjin **ricemyring: #stylus profited **TMM**
Search completed: June 22, 1999, 10:58:45 Job time: 144 sec
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OM protein protein search, using sw model

Run on: **Inne 22, 1994, 10 59 41 | Search time 45 16 Seconds (without alignments)

Title: US-09-030-061-2

Perfect score: 33

Sequence: US-09-030-061-2

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T4019 segs, 26640295 residues

Database: SwissProt_36:*
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Pred. No. is the number of results predicted by chance to have a score oreater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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AND WHILL PONNIGH M., CUESEN I., COUFER J., COULSON A.,

BEACH N. A. GREEN I. HARNIN H. FAVELLO A. FRASER A.,

TARTY & A., GREEN I. HARNIN H. HILLER L., JIER M.,

INSK M. KEPSHAW J. MIPSTEN J. LAISSTER N.,

INSK M. KEPSHAW J. MIPSTEN J. CANHARMER D. SHOWHEEN F.

HILLEM N. M. LAMITH M. A. SMITH M., CANHARMER F. STACEN F.

HILLEM N. M. LAMITH A. SMITH M., CANHARMER F. STACEN F.

HILLEM N. M. LAMITH M. MILKINSON SPROMAT J.,

KAN N. A. WEINEL N. WILKINSON SPROMAT J.,
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EMEL: Z2711b; G41590; -.
EMEL: Z2711b; G41590; -.
EMEL: Z3811, G486571; -.
P1K: S38154; S38164;
P1K: S39127; S39127;
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MUTAGEN
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CONFLICT
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NATURE 349:494-499(1991).

PHYSTORY INFLUENCES THE FIRELITY OF PRANCHESINI RECOGNITION IN PERSONAL THIS IS RNA-DEPENDENT ATPASE WHICH IS ESSENTIAL FOR VIABILITY IT MAY MEDIALE ONE OF HE MANY ALVEROUS HING STEED OF SPELICEUSUME ASSEMBLY AND THAT ACCURACY OF BRANCHPOINT RECOGNITION MAY BE COUPLED TO ATP BINLING AND/OF HYDROCYSIS.

"I STROCKLULAR TO OTHER "DEAD" HOX PANILY HELLOASES, BELLONGS TO THE "LEAH" SUBFANILY.
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Ol-JUN-1994 (REL. 29. LASI SEQUENCE OPDATE)
Ol-JUN-1994 (REL. 29. LASI ANNOTATION UPDATE)
PRE-MRNA SPLICING FACTOR KNA HELICASE PRP16.
PRP15 OK YKRUSSEW OF YKS405.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
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MEDILINE: 94562327.

GARCIA-CANTALEJO J., HALADRON V., ESTEBAN P.F., SANTER

REMACIA M.A., REVUELTA J.L., BALLESTA J.P.G., TIMENEZ

YEAST 10.231 245(1994).
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BURGESS S., COUTO J.R.,
CELL 60:705-717(1990).
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                                                                                                                                                                               373
386
473
698
                                                                   Conservative
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                                                                                                                                                                               869
                                                                                                                                                                                                380
386
476
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                                                                                    87.9%;
87.3%;
                                                                                                                                                           121652
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Pred. No. 43;
1; Mismatches
                                                                                                                                                         ATP (BY SIMILARITY).
Y->D: SUPPRESSOR PHEN TYFE.
DEAH BOX.
A -> R (IN REF. 1).
MW: E98TOFEB CRC32:
                                                                 Score 29; DB 1; Long's [07]; Prod. No. 89; [1; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 863:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SANTES M.A.
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RESULT 5
RAD4_YEAST

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RE SECTENCY ALGERY.

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ANGELY A. BRENNAN I CARPENTER J CHENRY J.M.

RA AVILES E. SERNI A. BRENNAN I CARPENTER J CHENRY J.M.

RA AVILES E. PUNCAN M. GUZMAN E HARTZELL G. HUNICKE-SMITH S.

RA HYMAN E PUNCAN M. GUZMAN E HARTZELL G. HUNICKE-SMITH S.

RA MOSEDALE E. NAKAHARA K., NAMATH A., NORGREN R., OEPHER P., OH G.,

RA MOSEDALE E. NAKAHARA K., NAMATH A., NORGREN R., SHOGREN I., SMITH V.,

RA PETEL E.X. ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,

RA PETEL E.X. ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,

RA PETEL E.X. ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,

RA PETEL E.X. ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,

RA PETEL E.X. ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,

RA PATION D. WET Y YELTON M. ROTSTEIN D., DANTS R W.

SUMMITTED (DECISION IN MICLETIFICE EXCISION FEDALE GE ENA CAMACHE

CC CITACTION. LAVOLVED IN NUCLEAR.

CC TISCHERE D. MICHAEL STORM STORM SUME, TO MAMMALIAN XP.

DR EMBL, MICASSO (272330 - 1)

DR EMBL, MICASSO (272330 - 1)

DR EMBL, MIGASSO (272330 - 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Incal
Matches
              REDM_YEAST STANDARD: PRT: 1351 AJ
P13433;
C1-340-1990 (REL. 13, CREATED)
C1-740-1990 (REL. 13, LAST SELVENDE HEDATE;
O1-NOV-1990 (REL. 22, LAST ANNOTATION URDA;
DNA-DIFFOREN ANA POLYMERASE MITOCHONDRIAL I
RPC41 OR YELOSON,
SACCHARMYONE OFFICESTAE PRAYERS YEAST)
SACCHARMYONE OFFICESTAE TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAD4_YEAST STANDARD,
P14736;
Q1-APR-1990 (REL. 14, CRE
Q1-APR-1990 (REL. 14, LAS
Q1-QTT-1996 (PEL. 14, LAS
Q1-QTT-1996 (PEL. 34, LAS
DNA REPAIS FEDERN RAD4,
PAD4 OP MEPIAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FR.M N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIO L.B., ER
BACTERIÓL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1058: RAD4.
S. CNA-BINDING: NUCLEAR PROTEIN.
250 POTENTIAL.
250 VCI -> EGL (
223 205 VCI -> EGL (
754 AA: 87174 MW; BE655EF2 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EEB-1993)
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L. 171:1862:1869(1989)
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33 - 33 9
34 9
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                                                                             CREATED)

LAST SELVENCE MEDATE)

LAST ANNOTATION UPDATE)

YMERASE MITTOPHONDETAL PRECUESOR
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Fred. No. 61:
1 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANNOTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
VCI -> EGL (IN REF.
; PE65DEF2 CRC32;
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된
터
                    HEMIASCOMMUNICE
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|-| 4
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                                                                                                        (EC
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CHERRY J.M.
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TOEA_YEAST
ID TOEA_YEAST
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                                                                                                                                                                                                                                                                                       RESULT
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Book Local Similarity 83.28,
Matches 5; Conservative
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MEDLINE: 88002333.
MASTERS B.S. STOHL L.L..
CELL 51:89-99(1987).
[2]
SEQUENCE FROM N.A.
RIEGER M.;
STEMITION (MAS-1994);
-- HUMNITON SECURITS THE THE THA POLYMETASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
CONFILCT
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MEDILINE: 95405092.

MAITET M. HACIMARA H. SHIBATA T. CEAWA M. M. MURAKAMI Y. MAITET M. HACIMARA H. SHIBATA T. CEAWA M. M. SASANTAA M. TSTCHIYA Y. SOFDA F. YYROYAMA M., SASANTAA M. EXI T.;

MAT GENET. 16 261 266 (1995).

THE TRAINS HAA HEINE THE FULF PIRANGERSHEE PETPHESPHATES AS STHETRAIPS.
                                                                     MEDLINE: 95050500.

FEAVER W.J., HENRY N.L., BOSHNELL D.Z FEAVER W.J., KORNBERG R.D.:

J. E1.cl. CHEM. JEG: 27547-27553(1994).
                                                                                                                                                                  UI-JUN-1994 (KEL 29, CREATED)
01-JUN-1994 (FEL 29, LASI SEQUENCE UPDATE)
01-JUN-1994 (FEL 29, LASI SEQUENCE UPDATE)
TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TEILE-ALPHA)
(TRANSCRIPTION FACTOR A LARGE SUBUNIT) (FACTOR A 55 KD SUBUNIT)
TAIL OR YKLU28W
SACCHAPOMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                          1300 FEDITO 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: (*5 *1); (*1)* 4643;
EMBL: 544598; 0871937;
PIP: A07336; A27336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE) PS00489; RNA_POT_PHAGE_2; 1.
PFUSITE, PSUGPUD, KNA_FUT_FHAGE_1; 1.
CNA-CIFFITET RNA: FIRMFRASE, TRANSORT
                                                                                                                     STRAIN-BJ926;
                                                                                                                               SEQUENCE FROM N A
                                                                                                                                                       EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                 1 FEDMID
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SUBSTELLULAR LUCATION: MITOCHONDRIAL SIMILABITY: RELONGS TO THE PHAGE AN EAMILY.
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11189
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THIS TO THE INITIATION CLARKS.

THOSE TO THE INITIATION CLARKEN.

IN COTERMINAL COMAIN KINGS AND
                                                                                                                                SECTIONS
                                                                                             BUSHNELL D.A.,
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                                                                                                                                                                                                                                                                                                                                                                       Fred. No. 1.1e+02;
1: Mismatches 0
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BY SIMILARITY.
BY SIMILARITY.
S -> 2 (IN REF
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                                                                                                                               OF 55-71.
                                                                                             SAYRE M.H.,
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                                                                                                BRICKNER
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LIVIARE L. FALL W. MIDTLEAF (CF-BANLE).

LARTIES S. FALL B. MAMMALIAN IFITE-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRAPP P STATELIS M., PRICE 5.8
TIOS 451, 2016621 6629(1992)
TA VAY BUN TEL-MERIC 1404 SEUGENCES.
CLULAR LIKATION: NUCLEAR (PROBARLE)
ARGIY HEL-MOS 15 THE TELJMERETBINDING PROTEIN ALPHA SUBGNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 44 month 12
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                                                                                   ANOXYPHOTOBACTERIA: GREEN BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29: DH I: Length 482:
Fred. No. 38.
I: Mismatches 0: Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seore zu: DB l:
Pred. No. 36:
l: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOLY SHALL TROAD:
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                                   STRAIN-168;
                                                                                                                                                                                                                                                       YLON
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1:1:3555

ERRINGTON

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STRAIN=SZOOL,
MEDZINE, 9743481.
PRIPGEP M. PRUFCKNEP M., SCHAEFER M., M.
YEAST 13.1077:1090(1997).
# EMBL: 272597; E243961; -.
W HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
W HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 311 327 POTENTIAL
TRANSMEM 38/ AA, 44585 MW; BOF83B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.8
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5: Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGH5_YEAST STANDARD; PRT; 387 AA.
P53159;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LASI SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LASI ANNOTATION UPDATE)
HYPOTHETICAL 44.6 KD PROTEIN IN RPL6-HSF1 INTERGENCE HEGGEN
                                                                                                       15-JUL-1948 (PEL 36, CMEATED)
15-JUL-1948 (PEL 36, LAST SEQUENCE UPDATE)
15-JUL-1948 (PEL 36, LAST ANNOTATION UPDATE)
15-JUL-1948 (PEL 46, LAST ANNOTATION UPDATE)
HYPOTHETICAL 41.6 KD PROTEIN IN FMI-SFOVM INTERGENIC REGION
                                                                                                                                                                                                   YLON_BACSU
034617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEASI).
EUKARYOTA; FUNGI: ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00505; PEPCK_GTP; 1.

$\frac{2}{2}\text{SUBCNEW GENESIS: LYANE; JECANGAYLASE; GTF-BENGENIAL).} \

$\text{NP_BIND} \text{248} & 255 & GTP (POTENTIAL).} \

$\frac{2}{2}\text{ACT_SITE} & 299 & BY SIMILARITY.} \

$\frac{2}{2}\text{SUBCENCE} & 646 & AA: & 72531 & MM; & 45D273AH & CRC32.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                       BACILLUS SUBTILIS: PROKARYOTA; FIRMICUTES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      361 FEDQTD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 WEDMID 388
                                                                                                                                                                                                                                                                                                                                                                                 1 FEDMID 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $56812; E80941;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
83.3%;
                                          ENDOSPORE-FORMING RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Score 28; DB; Pred. No. 86; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28: DB 1: Length 487
Pred. No. 50:
0: Mismatches :: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
; BUF83B6D CRC32.
                                                                                                                                                                                                                        PRT:
                                                                                                                                                                                                                        363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUELLER - AUER
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                                          AND CONTENT BACTLLACEAR
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RESULT 12
CCH1_YEAST
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P50977:
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                                                                                                                                TRANSMEM TRANSMEM
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TRANSMEM
TRANSMEM
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PAIDHUNGAT M., DARRETT S.,

PALCHUNGAT M., TREGUES 6347(1997).

PALCELL BIGL. 17:6339-6347(1997).

PALCELL BIGL. 17:6339-6347(1997).

PALCELL BIGL. 17:637170N INTEGRAL MEMBRANE PROTEIN (POTENTIAL)

PALCELL BIGL. TO MARWALLAN SOLUTH AND DALGIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S2880,
MEDLINE: 97435491,
RIEGER M. HRUFCKNER M.
YEAST 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL) Y13937 E323524,
SUBTILIEST BG1389; YEDNI
HYPOTHETICA, PROTEIN
HYPOTHETICA, PROTEIN
                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE OALCIOM-CHANNEL FROTEIN.
COH! OR YGRA!7W OR G8501, CAKER'S
SACCHAROWCES CHERVISIAD (BAKER'S
EUKARYOTA, FORGI, ASCONYCOTIUM, HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRAIN-S288C;
MEDLINE; 9526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-001-1996 (REL. 34, CREATED)
01-001-1996 (REL. 34, LAST SEQUENCE OF
01-NOV-1947 (REL TELETINETTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.-!- SIMILAKITY: MELONGS TO THE UPF0063 FAMILY.
                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION
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                                                                     TRANSMEM
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                                                                                                         TRANSMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NE: 96267763.
FR AART O T M KI
12:385-390(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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691
766
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      \begin{array}{c} \mathsf{LL} \mathsf{LL}
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      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VICTAGE DATES CHANNEL
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RESULT 14
HDA1_CAEEL
TD HDA1_CAEEL
AC 017695;
DT 15-JUL-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDI1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š.
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RE SHOALNESSES / ABST2:

RE SHOALNESSES / ABST2:

RE SHOALNESSES / ABST2:

A DIFFRICH E. S. MUTITIAN I.T. HENNESSEY K.M., ALLEN E. AFAUTO R.,

A AVILES F. REPNO A. RENNAN I. CARPENTER J., CHEN E. CHERRY J.M.,

RA AVILES F. REPNO A. A. KOND C., LASHKARI D., LEW H., LIN D.,

PA CHUNG E. DUNCAN M., CUTMAN E., HAPTZELL G., HUNICKE-SMITH S.,

PA HYNAN R. KAYSER A., KOND C., LASHKARI D., LEW H., LIN D.,

RA HYNAN R. KAYSER A., KOND C., LASHKARI D., LEW H., LIN D.,

PA PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN II. SMITH V.,

RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN II. SMITH V.,

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RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMI S., SHOGREN II. SMITH V.,

RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMI S., SHOGREN II. SMITH V.,

RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMI S., ROBERTS D., SCHRAMI S.
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Pest Local Similarity 82.3
Pertugal 5. Conservative
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EMBL: $69371, G546371; -

EMBL: $169315, 3603275; -

EMBL: 9149315, 3603275; -

PIR: $44446; $44446.

$500: L0000699; $DI1.
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01-FEH-1995 (FEL. 31, LAST SEQUENCE UPDATE)
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SECRETORY PATHWAY PUT POT POT SACTIATION INHIBITOR.
GDIL OR SEC19 OR YED136W.
SACTHARMWOODS CEREVISIAL (BAKER S YEAST).
SACTHARMWOODS CEREVISIAL (BAKER S YEAST).
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EMBO J. 13:1718-1728(1994)
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***NCT N. BETS NISTBUE POR THE CEATETYLATION OF LYSINE RESIDUES ON THE N. THAT THE CORP. HISTORIES (H2A), H2B, H3 AND H4).

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search completed: June 22, 1999, 10:59:42
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GenCore version 4 5
Copyright (c) 1993 - 1998 Compugen Ltd.
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protein search, using sw model

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IL18 OR IGIF.
MUS MUSINUME (MUSEL).
EURARVITA, METAZOA, THORTATA, VERTERRATA,
EUTHERIA; RODENTIA.

TETEAN COAL MARRALIA:

SEQUENCE FROM N A AND TISSUE=LIVER; MEDLINE: 96061009 OPANDERA : TSTOTT H P TANIMOTO T TOTATION F

AND PARTIAL SEQUENCE.

POMATSU T., YUTSUDO M.,

HAKURA A.,

RESULT 1 IL18_HUMAN SIANDARD: PRT: 193 AA. ID IL18_HUMAN SIANDARD: PRT: 193 AA. AC Q14116: DI 15-JUL-1998 (REL 96 GREATED) DI 15-JUL-1998 (REL 96 GREATED) DI 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) DI 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) DI 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) DI (IFN-GAMMA-INDUCING FACIUR) (INIERLEUXIN-1 GAMMA) (II-1 GAMMA). Sucry Match 190.0%, Score 93, DB 1, Bost Local Similarity 100.0%; Pred. No. 0.8; Matthes 7, Confernative 0, Mishatches 0 EMBI, 140950, GI EMBI, 190434, GI MIM: 600953; -. SECTENCE CHAIN TISSUE*PERIPHERAL BLOOD: CONTI H FIN S J TINIL C. CHUN H.S. JOH T.H.: SURMITHAL (FEK-1997) TO EMEL/SENBANK, DDBJ DATA BANKS. SURMITHAL (FEK-1997) TO EMEL/SENBANK, DDBJ DATA BANKS. *** FUNCTION ACCRETE ANDUSAL MILLER CELL ACTIVITY IN SELECH CELLS AND SIMULATES INTERFERON GAMMA PRODUCTION IN THELIEN TYPE I MEDILINE: 90247546. USHTO S. NAMBA M. OKTPA T. HATTOPI K., NUKADA Y. TANABP F. KONISHT K. MICALLEF M., FUTII M., TOPIO FIKUDA S. IKEDA M. OKAMUBA H. KURIMOTO M.: BOMO SAPIERS (HOMAN). EUKAFYOTA, METABOA, CHOREATA, VERTEBBATA, TETBAPCOA, MAMMALIA: EUTHERIA; PRIMATES. PROPER CYTOKINE SEQUENCE OF 2-193 FROM N.A. SEQUENCE FROM N.A. IL18 OR IGIF. TISSUE=LIVER; IMMUNOL. 156:4274-4279(1996). CELLS io N in d 193 M. ...α ..α ..α 31405319; -. 31899242; -. 52323 × YUAK_BACSU Ell4_METJA INTERLECKIN-18. TEESETIT CROSS: BY SIMILARITY ALIGNMENTS ADA Y , AKITA K Longth 1980 £45914 pacilus su £57588 methanococc TANIMOTO T..

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NASS STATES INTERFERON GRAMMA PRODUCTION IN THELPER TYPE I
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                                                                                                                                                                                                                                                                    FILE
                                                                                                                                                                              TY A TIPVITY: ATE - KI, STORYTHY AMP + PYROPHOSPHALE.
                                                                                                                                                                                                      L. BETWERET J., TURCO B.:
+11+()+46).
N. HIAYS ESSENTIAL ROLES IN RECULATION OF CELLULAR
CSM OF CATALYSING THE SYNTHESIS OF A SECOND MESSENGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE PANTEDAS.
                                                                                                                                        TWINE TWILE
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45. LAST ANNOTATION UPDATE)
(ET 4.5.1.1) (ATE TYROPHOSPHATE-LYASE) (ADENYLYL
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85.7%;
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                                                                                                           LOTTE MW. DEASTOLD CROSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ.
                                                                                                                          POLY-SER.
PP2C-LIKE
                                                                  Score 32. DB 1, Pred. No. 15; l. Mismatches
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MET -> IS. (IN REF
46876979 18772).
                                                                                                                   CATALYTT
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                                                                                   Dength 2145;
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Query Match
Best Local Similarity
Teches 6: Conserv
  S & R C R C R C R R X R R R S C R E E E E
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-!- SIMILARITY: TO YEAST BUD3.
-!- CAUTION: IS INDICATED BY REF.1 TO BE A 3-IS-PUT CHEMPOPOSENASE (EC 1.1.1.85) (LEU2), BUT THIS EMBL; X79823: G791137: -.
SEQUENCE 379 AA: 4 4586 MW: 18CUIAG9 CMC32;
                                                                                                                                         01-FEB-1996 (REL. 33, GREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LASI ANNOIATION UPDATE)
HYPOTHETICAL 43.6 KL PROTEIN.
DEBARYOMYCES OCCUPENTALIS (YEASI) (SCHWANNIOMYCES (40THENIALIS).
EUKAFYSTA, FUNGI, ASCOMYCULINA: HEMIASQUMYCETES.
                                                                                                STRAIN=AICC 26077
MEDLINE: 95321019.
                                                                                                          SEQUENCE FROM N.A.
STRAIN=AICC 26077 / R91:
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 961/7562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (RFI 35, GREATED)
01-NOV-1997 (RFI 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (RFI 35, LAST ANNUTATION UPDATE)
CHROMOSOMAL PEPLICATION INITIATOR PROTEIN DNAA
                                                                             ISERENTANT D., VERACHTERT H.; YEAST 11:467-473(1995).
                                                                                                                                                                                                              P480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOPLASMA PNEUMONIAE. PROKARYOTA, TENERICUTES;
                                                                                                                                                                                                                          YLEU_DEBOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 97105885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEAIN-ATCC 19341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HILBERT H., HIMMELREICH R., PLAGENS H., HEREMANN NUCTEIC ACIDS RES. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                      TO BE A 3-IS-PROPYLMALATE
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Query Match Best Local Similarity

90.9**%**;

Score 30; Fred. No.

DB 1;

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P21421;
01-MAY-1941
01 JCT 1996
01-NOV-1945
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                                                                           MEDILNE: 96107345.

AROUTE H. J. GILDMAN N. BARNETT P. MOOFE P.W. I.
SIFATH M. J. WHYTE A., WILLIAMSON D.H., WILSON R.J.M.
MCC. BIOCHEM, FARASITOL, CC.LL. LO. (1394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANN/TATION TERATE)
17-JUL-1998 (REL. 36, LAST ANN/TATION TERATE)
1NTERLEUKIN-18 PRECUPSOP (IL-18) (INTEPPEPON-GAMMA INDUCING FACTOR)
(IEN GAMMA INCIDING FACTOR) (INTERFEUKIN-1 GAMMA) (IL-1 GAMMA)
1L18 OR IGIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LV4_84"II
                                                                                                                                             PLASMODIUM FALCIPARUM EUKASYTTA PROTIZIA /
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CONTI B., JAHNG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGUENCE FROM N.A. STRAIN-SERAGRE-DAMIFY: TISSUE-ADRENAL GLAND:
        SEQUENCE OF 328-1024 FROM N.A. MEDIINE: 91187055.
                                                                                                                  STRAIN-BW
                                                                                                                          SEQUENCE FROM N A
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EUTHERIA: RODENTIA.
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FUNDITON, AGGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STINGLATES INTERFUSEN GAMMA PRODUCTION IN I HELPER TYPE I
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LAST ANNOTATION
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2: Mismatches
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MISSING (IN ISOFORM &
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- THIS BEAM PRIVICENCE IS ENCORED BY A CIRCULAR CHAINE TO THE RNA POLYMERASE BUTA CHAINE EMBL: X75544 G887604; -.

R EMBL: X75547 G9880; -.

R EMBL: X52177 G9880; -.

R EMBL: X95275; ENCORED TO THE RNA POLYMERASE BUTA CHAINER FOR STOCKER PROGRET BUTA CHAINER PROSITE: PS01166; ENA_POL_BETA; 1.

PROSITE: PS01166; ENA_POL_BETA; 1.

YOUR SECTION OF THE CHECKER PROGRET BUTA POLYMERASE.
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Bost Local
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01-001-1996 (REL. 34, CREATED)
V1-001-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
FROBABLE LEGGYL-HANA STWIRLIASE (EC 6.1.1.4) (LEUDINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _CAEEL
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                            CAENORHABUITIS ELEGANS.
EURAFTOTA, METACOA, ACCELLMALES
                                                                                                                                                                                                                                                                                          SHEWITTED (NOV-1994) TO EMBI/GENEANK/DOBI
                                                                                                                                                                                                                                                                                                                                                       GARDINER A.;
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    CATALYTIC ACTIVITY: N NUCLEUSIDE TRIPHUSEHATE

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35, LAST SEC
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Pred. No. 43;
C: Mismatches
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Prod. No. 77;
I. Mismatches
                                                                                                                                                                                                                                                                                                                                           THE STREET STORY
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프리트리즘 중국무 모두모
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AAFIL BLOWNS I. PEFTIDASE FAMILY M20A; ALSO KNOWN AS THE APPLANY (FILEWARD). FAMILY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.12.13
                                                                                                                                                                                                                                                                                                                                                                                                           III A TIVITE AND SHIKIMALE * AUP * SHIKIMALE 3-PHOSPHALE.

III A TIVITY EHRSEHGEN (LPYRUVATE * 3-PHOSPHOSHIKIMATE *
HIGHBLE * O(*) (1 "ARBOXYVINVL) * 3-PHOSPHOSHIKIMATE
Y SET *WILLIE STEED IN THE HIGSYNTHESIS FROM CHORISMATE
AS MALL AMILY AND ATOM (THE SHIKIMALE PATHWAY).

IN HIGH 2: **
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N: THE PRESENTE PRIVATE ARRAY ARABINO-HEPTULOSONATE =
THE VELVE OF THE SHOP OF DECXY-ARABINO-HEPTULOSONATE =
THE VELVE OF THE SHOP OF TAXALE OF THE VELVE OF
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(BEL C. TREATED)
(BEL C. LACE ARRESTATION OFFARE)
(BEL C. LACE ARRESTATION OFFARE)

NALOE MELTIFETTIE (CONTAINS CONTAINS 
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ALLES TEIN: HYDROLASE; METALLOPROTEASE
1 - AAL 44804 MW; C7FC81DE CRC42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 DEHYDROUTHASE_1; 1.
112 SHIKIMATE_KINASE; 1.
113 SHIKIMATE_KINASE; 1.
114 TIL SHIKIMATE_KINASE; 1.
115 SHIKIMATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARTSTELD ALE., ALLEN ALG., MASKELL D.J., PETERS S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SENTILLTUES: SCOTOBATTERIA: FACULTATIVELY ANAFRORIC POISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEEV 1
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                                                                                                                                                                                                                                                                                                                                                                     EPSP_SYNTHASE_1.
                                                                                                                                                                                                                                                                                                                                    EPSP_SYNTHASE_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOT YET CLASSIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139:2901 2914(1993)
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIRESHORED CONYANABINOTHEPTULOSONATE FIRESHORESHIKIMATE HI(2)CLEURINATE GRAFICE)

LHIFUMATE GRAFICE) SEHYDRUSHIKIMATE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                    EPSP SYNTHASE
*-DEHYDROQUINASE.
                                              SHIKIMALE KINASE.
                                                                                                                     3-DEHYDROQUINATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>.</del> .
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RESULT 11
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Bust Dival Similarity Strong
Totolog 5, Conservative
                                                                                                                                                                                                                                    RESULT
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Bost Local Similarity (...
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ACT_SITE
NP_BIND
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                            PLANT PHYSIOL. 104:755-756(1994).

PLANT PHYSIOL. 104:755-756(1994).

SIMILARITY: BELONGS TO THE CYTOCHROME P45 FAN EMPEL. 124128.

STORMED STORMED STORMED P459; 1.

PROSITE: PSONORA: CYTOCHROMEDP459; 1.

OMIGGRIGGIASE: ELECTEON THANSPORT: HEME. (BY SIMILARITY)
METAL 436 436

METAL 436 AA; 55387 MM; 4A36290B CRC32:
           GRANDI G.;
MICHOBIOLOGY 141:645-648(1995)
-!- COFACTOR: CONTAINS A COVAL
                                                                                                                                             U1-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, IAST SEQUENCE UPDATE)
15-JUL-1996 (PEL. 36, IAST ANNOTATION UPDAT
PEPTIDE SYNTHETASE 2.
                                                                                                                                                                                              PFS2_EA
                                                                                                                                                                                                                        _BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (REI. 34, CREATED)
01-FEB-1996 (REI. 38, LAST SEQUENCE UPDAIE)
15-JUL-1998 (REI. 36, LAST ANNOTATION UPDAI
CYTOCHROME P450 LXXIB1 (EC 1.14.14.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1052 FSLILKK 1058
                                                                                                                      BACILLUS SUBTILIS
                                                                                                                                    PPSB OK PPSZ.
                                                           MELLINE,
                                                                        STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UDVARDI M.K., METZGER J.D., KRISHNAPILLAI V., REACHE W.T., DENNIS E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPPARALES: CRUCIFERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGLOSPERMAE: DICCIYLEIMMEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P49264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C71B_THLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SHOOT APEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THLASPI ARVENSE (FIELD PENNYCRESS
                                               OGNONI A., FRANCEI E.,
                                                                                                                                                                                                                                                                      348 FKLVLKE 354
                                                                                                                                                                                                                                                                                              1 FKLILKK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FKLILKK 7
(POTENTIAL).
                                                                                                                                                                                                           FVCEA
                                                          95327362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1217 1217 FORMS A SCHIFF-BASH INTERHEDIATE (BY SIMILARITY).
1581 AA; 178043 NW; B914BECC CRC*2:
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822
875
1189
1217
                                                                                                            FIRMICUTES
           CONTAINS A COVALENTLY BOUND PHOSPHOPANTETHEINE
                                                                                                                                                                                                           : TANUARU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                36. LAST ANNUTATION UPDATE)
E 2.
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827
1189
1217
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71.4%;
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                                                                                                         ENDOSPORE-FORMING RODS AND COURTE BACILLALEAD
                                                                                                                                                                                                                                                                                                                                Score 28; DB 1; Length 496; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2d: DB l: Longth [58]
Fred. No. 98;
0: Mismatches [: Indels
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Best Local Similarity
Matches 5; Conser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       __YEAS;
SRB4__YEAS]
P32569;
P32569;
01-00T-1993 (REL. 2
                                                                                                                                                                                                                                                  SUBMITTED
                                                                                                                                                                                                                                                                                          SEQUENCE FOR ALL STEAM S.T., HENNESSEY K.M., ALLEN E., ARAUJO R DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., GRERRY J. AVIIFS F. REPRA A. BRENNAN T. CARPENTED G., HUNICKE-SMITH S., CHUNG E., FUNCAN M. GUZMAN F. HARTIFIT G., HUNICKE-SMITH S., HUNICKE-SMITH S., FUNCAN M., FANGER A. F. WE T. LAGRAFI G. LEW H., LIN D., WOSEDALE D. NAKAHARAK MAMATH A., NORGPEN F., GERNER P., OH G. MOSEDALE D. NAKAHARAK MAMATH A., NORGPEN F., GERNER P., OH G. MOSEDALE D. NAKAHARAK MAMATH A., NORGPEN F., GERNER P., OH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                     THOMPSON THE
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SK_TENTE
                                                                                            EMP!
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PROSITE: PSC0455: AMP_BINDING: 2.
PROSITE: PS50175: ACP_DOMAIN: 2.
PROSITE: PS50175: ACP_DOMAIN: 2.
PROSITE: PS50175: ACP_DOMAIN: 2.
PROSITE: PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: Z34883; G599469;
EMBL: Z99113; E1183491;
SUBTILIST: BG10971; PPS
                          NUCLEAR PROTEIN
                                                 FIR. A40711. A40711.
TRANSEAC; T02148; -.
SGD: L0002051: SRB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Z28;
MEDLINE: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRB4 OR YER022W
SACCHAROMYCES CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (REL 33 LAST AN SUFFREERS F F SHA PTIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARTOTA
                                                                                                                                                                                                            ET F X DORFFTS TO SEHT P SCHPANM'S, SHOGREN I, SMITH V , LOR P. WEITEN DETTEND N. DAVIS R.W. ; SMITH V , WITTED (DET-1994) TO FMAI NEWBRANK/DEBI DATA FANKS
FUNCTION: TRANSCRIPTION FACTOR THAT HAS AN IMPORTANT ROLE IN BASAL AND INVALCE TRANSCRIPTION IN VITE AND IS ESSENTIAL FOR EFFECTENT ESTABLISHMENT OF THE TRANSCRIPTION INSTRATIATION APPRAATUS THE SKB-TRE COMPLEX SINES SPECIFICALLY TO THE C-TERMINAL DOMAIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATR-DEPENDENT COVALENT RINGHAM OF AME TO THEIR SUBSTRATE
                                                                                            SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
L: L10126: G172693: -.
(- M19778: G603614. -
                                                                                                                                                                  SUBUNIT: SFR2 SPR4. SPR5 SPR6 AND A POPTION OF CELLULAR THE AFE
                                                                                                                                                                                                                                                                                                                                                                                                                                  73:1361-1375(1993).
                                                                                                                                     COMPONENTS OF A HIGH MOLECULAR WEIGHT MULTISUBUNIT COMPLEX THAT STIGHTLY BOUND TO PHA POLYMEPASE II.
                                                                                                                                                                                              POLYMERASE II (CTO) IN FORMING THE TRANSCRIPTION INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    970
2041
2041
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FUNCI: ASCOMYCOTINA: HENTACTO
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- 2017 ATY
1 2041 PHO
- AA, 290101 MW,
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T (AST SECTENCE TEDATE)

3. LAST ANNOTATION OPDATE)

TOWERASE E SER4
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ACYL TARRIER (ACP).
PHOSPHOPANIETHERINE (POLENIIAL).
MW. FEAAACEF (POLE).
         G->C: GAIN-OF-FUNCTION SUPPRESSION 4501=EF10 75/32)
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pred No 1 6e+02:
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                                            Matches
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                                                                                                                                                                                                                                                               MEDLINE: 95401276.

BACST S., RIM S., MALEGNAGG E., TONG E.I., REINSERG D., IKURA M.;

CELL M2:857-887(195).

-1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION

OF FUNKAPYOTIC GENES TRANSCRIBET BY PNA POWYMERASE IT.

-1- SURGULII. ASSOCIATES WITH TELLINIA (PAR POWYMERASE IT.

TIA-ITS (FAR-COMPLEX) WHICH IS THEN RECOGNIZED BY POLYMERASE IT.

TIA-ITS (FAR-COMPLEX) MICHEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OUU403;

U1.EEC-1932 (REL. 24, CREATEU)

O1-DEC-1992 (REL. 24, LASI SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

TPANSCRIPTION INITIATION FACTOR IIB (TFIIB).
                                                                                                          REPEAT
                                                                                                                                                                                                                     :: SIMILARIT: BELONGS TO EMEL: N59258: 337058; -. EMBL: N76756; 3339490; -. PIP: S17654; S17654.
                                                                                                                                                                                                                                                                                                                                                                                                              X-FAY DEFINALLUSEARRY (2.7 ANGSTRUMS) OF 111-316 MEDLINE) 95405464.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 92052130.
MALIK'S HISATAKE K
FREE MATE ACAD SE
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                                                                                                                                                                                                  PDB; 1VOL; 08-NOV-96.
PDB; 1TFB; 12-MAR-97.
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                                                                                                                                                                                                                                                                                                                                                                                        NIKOTOV D.B., CHEN H., HALAY E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HA I., LANE W.S., REINBERG D.;
NATURE 352:689-695(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A MEDLINE; 91342994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN)
EUKARYOTA, METAZGA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTF2B OR TFILE OR TF2B.
                                                                                                                                                     TRANSCRIPTION RESTLATION:
                                                                                                                                                                                       TRANSFAC
                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 111-316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                          SD-STRUCTURE.
311111 SET
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                      1 FELLLE 6
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5; Conserv
                                           6; Conservative
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218
216 AA;
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349??
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                                                                                                                                                                                                                                                                                                                                                                                        PUBLEY S.K.;
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BENTALL OF MELLATION PACTOR LIB (TETLB) (RMA POLYMERASE II

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FS. Claim.) Faue 46: 60pp; English.

CO. (161F-2). An 161F-2 variant (#217F2) and an 161F variant (#21049).

CO. (161F-2). An 161F-2 variant (#217F2) and an 161F variant (#21049).

CO. the negligible acid sequences can be used to quantify the expression of the negligible acid sequences can be used to quantify the expression of the farmy filles that are associated with inflammation or aberrant party in a 171F-2. The protein as antibodies, antagonists or other contability interpression as antibodies, antagonists or other contability in the protein can also be used to diamnze protein or expression or activity. The protein can also be used to diamnze protein or trait 181F-2 if duction if protein also be used to diamnze protein associated with inflammation.

So Sequence 193 AA:
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Cooks BC, Coloman B, B
WPI; 97-368677/33.
                                                                                           W46592:
23. MAY 1998 (fise entry)
Amino acid sequence of human interleukin-1-gamma.
Amino acid sequence of human interleukin-1-gamma.
Interleukin-1-gamma, It-1-gamma, mouse, cytokine: IGIF, interleton-gamma:
induction; antikody: disposetto assay, fusion protofn, cotivity;
immunological disorder: allergy.
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20-EEC-1996: U20422.
29-DEC-1995: US-580667
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14-JAN-1998 (first entry)
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Therforen gamma inducing factor:2, IGIF:2, levelsyte: lymphocyte;
inflammation, proliferation, differentiation; maturation, tissue damage:
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                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  W46592 standard; Protein; 193 AA
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Location/Qualifiers
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Section of represents human interleukin-l-gamma (II-l-gamma) | 185 the human equivalent of a mouse cytokine, IGIF, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Latta ? palka."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         indels
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Rest Tocal Similarity
Matches 197, Conserv
                                                                                    Human; interleukin-18; IL-18; osteoclast; hypercalcaenia; osteoporda: osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis chronic freumatoid arthritis, deformity ostitis; primar, hyperthyrolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGIFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, thereglosis, solid malignant tumbours (e.g. femal carcinoma), rheumatism, osteoporosis and thrombepenia caused by radiation—and chemo-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues are replaced with different residues it is away from the consensus sequences shown in W48956-W4898. The mutant IGIFs are capable of stimulating immunocompetent cells for the production of interferen games and are claimed to be less todic, mor active and stable than the corresponding wild type IGIF. The movement is the area discretioned to enhance killer cell corrections and/or induce killer cell formation, and may therefore be useful as antitumour agents, antitumour agents, antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutants of interferon-gamma inducing polypeptide - useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents Claim 3: pages 36-37: 59pp: English.
The present sequence represents the wild-type human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild-type human interferon-gamma inducing factor. Interferon-gamma inducing factor, Interferon-gamma inducing factor, Interferon-gamma, killer cell; interferon-gamma inducing factor, Interferon-gamma, killer cell; interferon-gamma inducing factor, income, killer cell; interferon-gamma inducing cell; interferon-gamma inducing cell; interferon-gamma inducing cell; interferon-gamma inducing factor.
                                           Homo sapiens
EP-861663-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducing factor (INTE) the invention provides for mutant human and mouse interferon-gamma inducing factors in which one or more cysteine residues are replaced with different residues at a way from the consensus sequences shown in W48956-W48858. The mutant likes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 "NOV-1997; JP-329715.
29-NOV-1996; JP-333037.
21-JAN-1997; JP-020906.
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03=JUN-1998.
28-NOV-1997; 309632
                                                                                                                                                               Human interleukin 18
                                                                                                                                                                                                                                      W77077 standard, peptide, 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                      16-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kurimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          61 AVTISVKCEKISTLSCENKIISEKEMNPPDNIKDTKSDIIFFGRSVPGHDNKMCFESSSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 YFGKLESKLSVIFNUNDOVLFILOGURFLFEDMTDSDCRDNAGKTIFIISMYKUSOPROM - «
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YEGKLESKLSVIRNINDØVLFIDØGNRPIFEDMTDSDØRDNAPPTIFIISMYKDSØFRGM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVTISVKORKISTI SORNKI ISEKEMNEDDNIKETESPIIFE JESVESHI NEMJEBSSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consent vallive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 816; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            indels
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02-SEP-1998. 24-FEB-1998: 301352

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Best Local
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02-SEP-1998.

04-FEB-1998.

05-FEB-1998.

05-FEB-1998.

07-955468.

CHAYE - HAVASHTBARA SELEUTSU KAGAKU
Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
WPI_98-448964/39.
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Claim 4; Page 18: 56pp: English.

Interleable 19: (TU-18) or a factional equivalent can be used for inhibition of esteporast formation. IL-18 is used for treating or presenting esteporast related diseases e.g. hypercalcaemia, esteporable behoet's syndrome, esteposarcoma, arthropathy, chronic rheumatoid arthritis deferming the content of the content o
                                                                                                                                                                                                                                         of e.g. Appercallmenta, isterclasiona, Behoet's syndrome, osteosascoona, chronic rheumatoid arthritis, deformity ostitis, primary apperthyroidism and osteoporosis of the east of the primary appearance of the figure of the control o
                                                                            Thibition of estendast formation. This is used for treating of preventing esteoclast related diseases e.g. hypercalcaemia, esteoclastoma Beher's modified assertances, arthropoly, elevate thought if arthrotis, deformity estitis, primary hyperthyroidism, esteopenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                 C 4 40 0
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Interleakin 18 active profess osteoclast; hypercalcaemia; osteopenia;
Human; interleukin:18: IL-18: osteoclast; hypercalcaemia; osteopenia;
osteoclastica echoetis syndiche, osteocsarcomi, arthropathy, osteopenosis,
ohronia chesmatold arthritis: deformity ostitis; primary hyperthyroidism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillespic MT Hora WPI: 98-448964/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W77082 standard. Protein: 193
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les 157: Consert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-18 to inhibit osteoclast formation - in treatment
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        193 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /bote: "Signal peptide"
37. .193
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10-NOV-1995;
15-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IEN.gamma) produc by immunocompetent cells is the product of a phage cDNA clone (T22411) derived from a bunna liver library.

FOR amplification of the cDNA (see also T22409 10) and expression in Escherichia coll XI I Blue MRF Kan allowed productor inducer protein. This was used to construct hybridoms H 1, which produced anti-TEN-gamma inducer protein monoclosed artibody H-ImAb, useful in the detection and purification of the inducer protein (see also R09558).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interferon-gamma inducer protein.
Interferon gamma inducer protein, IFN-gamma; antiviral: virucide: antitumour; antibacterial; immunoregulator; adoptive _mmunotherapy.
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23-FEB-1995; UP-058240.
10-MAR-1995; UP-078357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel human protein (R99564) that induces interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example B-1-1; Page 28; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
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29-SEP-1995; JP-274988.
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Fukuda S, Kohno K, Kunikata T, Ku
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Ljuvi I.
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tenso inducer protein; IEN-damma; antiviral; virucide.
                   THE REPORT LABOR
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Fred. No. 1.7e 82;
p: Mismatches 1
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  TAND AND SELECT OF AND SELECT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overy Match 99.4 Bost Local Similarity 99.4 Matches 156: Conservative
24 JAN 1996;
04-007-1908;
10-MAP-1995;
29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mature portion of a novel human protein (R9950) induces interferen gamma (IN adamma) prode. By immune appetent cells is the product of a cNA chame (IN24A) which from a human liver library. The protein enhances the exphonancity of killer cells and/or induces the formation of killer cells (c.a. M. cells, lymphokine-activating killer (IAK) cells, and hytotaxic Trocks). The mature protein (see also R9958) is useful as an antiviral antitumor, antibacterial, immunoregulatory and blood platelet enhancing agent, and can be used in adoptive immunotherapy. It is sequence 193 AA:
                                                                                                                                                                                                                                                                                  viral disease; bacterial infection; immune disease
                                                                                                                                                                                                                                                                                                          Human protein for induction of interferon-gamma Interferos gamma, immunuoumpetent cell; mallynam
                                                                                                                                                                                                                                                                                                                                                                                                   W24258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-1994; JP-304203; 23-FEB-1995; JP-058240; 10-MAR-1995; JP-078357.
                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                          W24259 standard; Protein; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding interferon-gamma prodm.-inducing polypoptide to treat and prevent, e.g. viral disease, maliquancies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAVE) HAYASHIBARA SELBUTSU KAGAKU.
Fukuda S. Kohno K., Kunikafa T., Kun
Taniguchi M. Tanimoto T., Toriqoe K.
WEI. 36.252837,726.
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                                                                                                                   17-JUN-1997
                                                                                                                                          J09157180-A.
                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 EGYFLACEKERDIFKLIIKKEDELGDESIMFTVONED 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Page 41-42; 48pp; English
JP-279906.
JP-079357.
JP-274988.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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JF 274988.
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                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                     /note- "Encoded by AYT"
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ଏହା . 4 ୭ :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Fred. No. 2.20-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karimoto M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
Best Local :
The present sequence represents a newel protein from human cells, which induces interference gamma (IRN wamma) production in immunocompetent cells. This protein enhances optoboxicity of killer cells and induces their formation. It is used as an antioncotic agent for antitumour immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and in the treatment of atopic or immune system diseases, e.g. asthma, haytever or rheumalism, when formulated with interleukin-3, it is also used to treat leukopaenia and thromborytopaenia associated with radiotherapy or chemotherapy of leukaemia and other cancers. When used in antitumour immunotherapy of leukaemia and other cancers. When used immunotherapeutic effect of interleukin-2 (IL-2), compared with use of IL-2 alone—either when administered to the medium in which cells (intended for return to the patient) are being grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1: Page 9: 12pp: Japanese.
This sequence represents a protein which induces interferon-gamma production in immunocompetent cells. This protein may be used as production in immunocompetent the prevention and treatment of the major component in a drug for the prevention and treatment of e.g. maintaint tumours, Thrai diseases, bacterial infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 9
                                                                                                                                                                                                                                                                         Human protein that indeeds interferor-gamma prode in information color cells useful for adoptive immuno therapy of tumours and as antimicrobial agent etc.

Claim 3, Fage 20 25pp. English
                                                                                                                                                                                                                                                                                                                                                       THAYB I HAYASHIRABA SETRUTSU KATAKU
AKITA K. ENGIT M. KULIMOTO M. NUKUBAY. Tanimoto
MPT: 40-200004,714
                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1996; 336997.
20-SEP-1996; JE-269105.
26-SEP 1995; JE-270726.
29-FEB-1996; JE-267474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-767178-A1
09-APK-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon gamma inducer protein.
Interferon gamma. IFN gamma: antiviral; antioncotic: radiotherapy; immunoregulatory; antitumour agent; chemotherapy; loukepagnia; thrombocytepagnia; immunocompetent cell; asthma; hayfever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A drug containing a polypoptide which induces interferon-gamma useful for treating e.g. malignant tumours, viral, bacterial o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W15701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGYFLAGEKERDLEKLILKKEDELGDRSIMFTVQNED 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVITIAVETEK FILISTENETISEKEMNPERMIKETKSDITEELESVPOHDNKMEEESSSY 120
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97-369391/34.
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Se 157 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ile. Thr
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                  Interferon gamma (IN yamma) production in immunocompetent cells. The pretein has high biological activity, including enhancing optomicity of killer cells and indiving Killer cell formation, in addition to inducing IEN gamma production by immunocompetent cells when expressed in mammalian cells, facilitating its use in low discages to treat/prevent, e.g. muliginant turnits. That or bacterial infections and immune diseases. As it is expressed in mammalian cells, it also has low toxicity when used in human treatments, minimising side effects. The DNA chooling the protein can be used in gene theretapy, e.g. by injecting vectors containing the UNA or transplanting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                       malignant tumours or viral diseases
Claim 2: Pages 49-50: 74pp; English
The present sequence is a protein, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    denomic FNA encoding polypeptide inducing production - by immuno-competent cells, us
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WFI; MM-064F14,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference 109
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Interferon-gamma; TEN-gamma; production inducer; game therapy; immunucumpetent cell; treatment; prevention; malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1998 (first entry)
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Sequence
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Kuilmuto M, Okura T, Torigoe K;
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Pred. No. 1.7e-82;
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Fred. No. 1.7e 82)
; Mismatches 1
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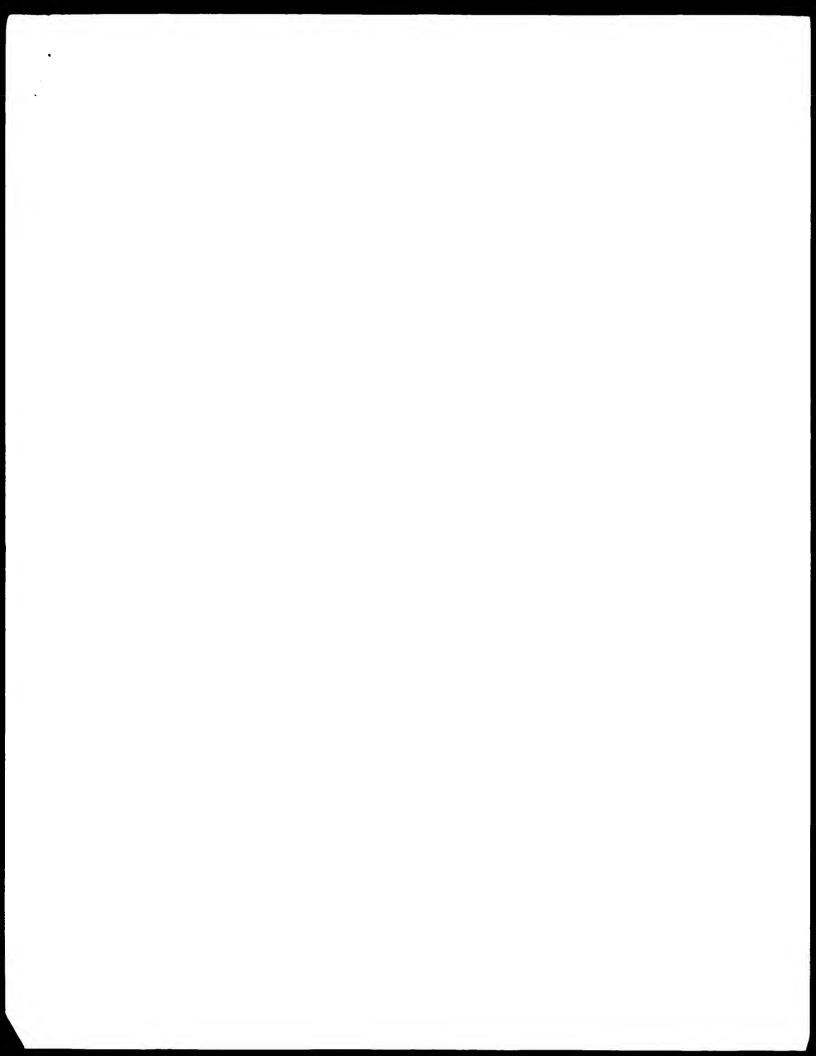
Bost Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 156:
             enzyme (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma a useful biologically active substance, chancing cytotoxicity by and importing the formation of eller reliability.
                                                                 Claim 5. Page 15: 18pp; English.

This is the amino acid sequence for the interferon darma (IEN-damma) inducing active protein which is cleaved to form the active mature protein when it is in contact with interleukin) beta converting
                                                                                                                                             Conversion of interferon inducing polypeptide precursor to active polypeptide - comprises use of interferon-1-beta-converting enzyme useful for e.g. enhancing cytotoxicity by killer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interferon gamma inducing precursor peptide: IFN-gamma: Interfeokin 1-beta-commetting engine, ICE, egit with a hiller antityinal agent; antitumour agent; immunopathy agent; antiseptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the precursor of an interferon damma (iEN-normal) inducing polypeptide. The polypeptide induces (EN-gamma production in immunocommentent colls (the polypeptide is not named but is described in it 12126,96 and 18469/96. An entyme can convert this precursor form into its active form by clearing a linkage between Asp at amino acid position 36 and Tyr at arice acid position 37 of its N terminal fragment. The entyme can be obtained from a human hacmatypoint; coll and can be
                                                                                                                                                                                                                                                                                    18 JOL 1997; 305276.
31-JAN-1997; JP-031474.
15 JOL 1996; JF-213267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W37741;
07 JUL:1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-1 aspart-l-al. The enzyme can be used for cleaving a tecombinant ITW axima pro polypeptide to form a mature polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide-processing enzyme interferon-inducing polypeptide Claim 3: Page 15: 18pp; English
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30-MAY 1997; JP-156062.
19-JUL-1996; JP-207691.
 polypeptide may potentially be used as an antiviral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kurimoto M, Tanimoto T;
WPI, 98・678838768.
                                                                                                                                                                                                             N-PSDB; V18906.
                                                                                                                                                                                                                                                Kurimete M. Tanimete T;
                                                                                                                                                                                                                                                                  (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                            28-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference
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Fred. No. 2.2e-82;
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Best Local Fir
Matches 156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-821005-A2.
28-JAN 1998.
18-JUC-1998: 305376.
31-JAN 1997: JP-031474.
20-JUL-1996: JP-210267.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conversion of interferon-inducing polypeptide precursor to active polypeptide - comprises use of interferon-i-beta-converting enzyme, useful for, e.g. enhancing cytotoxicity by killer cells (lbim 2; pages 14-15; 15pp; English. This is the amino acid sequence for the interferon-gamma (IFN-gamma) inducing precursor peptide, which is cleaved to form the active mature protein when it is in contact with interleukin-1-beta-converting enzyme (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma a useful biologically active substance, enhancing cytotoxicity by, and inducing the formation of killer cells. The polypeptide may potentially be used as an antiviral, antitumour and immunospathy ugent and as an antiseptic.
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W37740;
07-JUL-1998 (first_entry)
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Interferon-gamma inducing precursor peptide; IFN-gamma;
Interferon-gamma inducing precursor peptide; IFN-gamma;
Interferon-interferon-gamma inducing precursor peptide; IFN-gamma;
Interferon-gamma inducing precursor peptide.
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YPOYT FOYE SYLVAC HOLVELING CHEST ESSMISSIOPENMAPRITETISMYEDSQEEGM 60
                                                                                                                                       YEGK: ESKI SVIENI NIMOVIETIMONPPLEEDMIDSDORDNAPRITETISMYKDSORBSM 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98-088847/09.
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                                                                                                                                                                                                                                                                    Similarity 99.4
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Perfect score US-09-030-061-7 812 1 NFGPLHCTTAVIPN

Scoring table: BLOSUM62

NEGRIHOTTAVIPNINDOVI

...KKDENGDKSVMFTLTNLHQS 157

161830 segs, 20215318 residues

Database : A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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FI Mutants of interferon gamma inducing polypeptids (seful as antitumour, antiviral, antimicrobial or anti imminopathic agents proclaim 4, pages 38-99, 59pp; English, or anti-imminopathic agents proclaim 4, pages 38-99, 59pp; English, or anti-imminopathic agents are claim 4, pages 38-99, 59pp; English, or antiture things and confidence interferon gamma inducing factors in which one or more cystoline residues are replaced with different residues at or away from the confidence are replaced with different residues at or away from the confidence with incompletent cells in the production of interferon-gamma and are chalmed to be less toxic, more active and stable confidency and may therefore be useful as antitumour agents, antitumour immunopheriperities, will type mIGIF. The mutant mIGIFs are also chalmed to be useful as antiturous and antitumour agents, antitumour constituent because of the mutant mIGIFs are also chalmed to be useful for trouting hepatitis, or adjusted immunopheriperities, syndrome (ALDS), malutia, takersulosis, solid or first-peria caused by radiation, and chemo-therapy, extended so
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03-JUN-1998.
28-NOV-1997; 309632.
14-NOV-1997; JF-329715.
29-NOV-1996; JP-333037.
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25-SEP-1998 (first entry)
Wild-type mouse interferon gamma inducing factor.
Wild-type mouse interferon gamma inducing factor.
Interferon gamma inducing factor, interferon gamma, killer cell;
antitumour agent; antiviral agent; antimicrobial agent; tumour; mIGII
hepatitis; malaria, tuberculosis, renal carcinoma; rheumatism; AIDS;
osteep-tosis, thrombogenia acquired immunodeficiency syndrome.
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Kurimoto M, Okameto I. Yamamoto K;
WEI; 38:282-47,726.
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<u>:1</u> Ş 2 Ş Query Match 100.0%; Score 812; DB 1; Length 190; Best Logal Similarity 100.0%; Pred. No. 4.1c-77; Matches 101; Conservative 0. Mismatches 0, Indels 121 HELANGMEDHAEKITIKKKUENGEKSVMEILINLHOS 157 144 HELACOMEDDAFKLILKKKDENGDKSVMFILINLHOS 180 61 VILSVIGSKMSTLSGENKTIGEFEKGEPENIGGIGSGLIFFGERFEHENSHEGESSLIFG 120 \$4 VTI SVKESKMSTI SOKWKITSPREMORRENIODIO SDIJIFROVEVE GHNYMEFESSLIEG

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Example A 3-2; Page 36-37, 48pp, English.

A novel mouse protein (899559) induces interferon-gamma (IFN-dimma) produced by immunocompetent cells. Its sequence was deduced from that of a cDNA clone (132403) isolated from a mouse liver library. Recombinant IFN-gamma inducer protein can be produced in high yields using host cells, esp. Escherichia coli, transfermed with a vertor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein that induces damma interferon product is immunoccompotent cells - used e.g. as antiviral or antitumour agent, also induces cytotoxicity of killer cells claim 2: Page 22: 30pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1995; 308055.
15-NOV-1994, JE-304203.
23-FEB-1995; JE-058240.
16-MAR-1995; JE-078357.
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Mouse mature interferon gar
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                                                                                                                                                                                                                                                                                                                                                                          Fukuda S. Kohno K. Kunikata T. Ku
Taniquehi M. Tanimutu T. Torigoe K.
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                                                                                                                                                                                                                                               to treat and prevent, \phi_* q_* viral disease, malignancies
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29:SEF:1995, UE:174988
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a S. Kohno K. Kunikata T. Ku
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W24262 standard Frotein, 157 AA.
W24262;
15-007-1997 (first entry)
Murine protein for induction of interferousyamma.
Interferousyamma immunosompetent cell; malignant tumour;
Interferousyamma immunosompetent immune disease.
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04 707 1997, 10-2740000.
10 MAR-1006, 10-2740000.
20 SEP 1995, 1F-274000.
(HAYB, 1 HAYSSIFRIDA SECOTTST FATARET
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Disciplate Page 10:11 Tipp, Japanese.
This sequence represents a protein which induces interferon-gamma production in immunegomphish cells—This protein may be used as the major component in a drug for the prevention and treatment of e.g. malignant tumours, viral diseases, bacterial infections and
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Fred. No. 1.4e-76;
C. Mismatches 1, Indels
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18 Disclosure, Page 22, 25pc, English.

27 The present sequence represents a novel protein from mouse liver cells.

28 Which induces interferer gamma (IFN yamma) production in immunocompetent cells. This protein enhances cytoloxicity of killer oulls and induces couls. This protein enhances cytoloxicity of killer oulls and induces cells. This protein enhances cytoloxicity of killer oulls and induces couls. This protein used as an antionocitic agent for antifummour frame iterate, an artificity of limitating antifacts, or antifummour cells and in the treatment of atopic of immune system diseases, e.g. asthma, and in the treatment of atopic of immune system diseases, e.g. asthma, consider the remarkers when formulated with interlevkin-3, it is also considered to treat leukopaenia and thrombottopaenia associated with redictively for the immunethers; if leukaenia and their diseases. When used to the immunethers in the patient of the shell of the cells of the immunethers of the patient when administered to the patient of fixerial in the patient of the patient of the patient.
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WPI; 97-205381/
N-PSDB; T60536.
                                                                                                                                                           28-SEP-1998 (first entry)
Mouse IL-18 protein fragment.
InterleukhilB. IL 18, murium, treatment, autoimmune diseinmunosuppressant; inhibitor; receptor protein; detection
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Interferon-gamma inducer protein,
Interferon-gamma, IFM-gamma; antitytal; antioncotic; radiotherapy;
Immunoregulatory; antitumour agent; chemotherapy; leukopaenia;
thronto-ynopa-nia, immunocompetent cell, asthma; hayfever;
rheumatism; interleukin; killer cell.
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29-FER-1996;
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K, Fujii M. Kurimoto M, Nuk
                                                                                                                                                                                                                                                                                                                              standard; protein;
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Prod No 1 4e-76;
U. Mismatches 1. Indels
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       Matches
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28-NOV-1997; 309632.
14-NOV-1997; JP-329715.
29-NOV-1996; JP-333037.
21-JAN-1997; JP-020906.
Mutants of interferon-damma inducing polypeptide - useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents claim 6: page 44: 59pp; English.

The present sequence represents the mutant mouse interferon-damma inducing factor mIGIF/MUT11. The wild-type mouse interferon-damma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moting order interferencepames inducing factor NISHE, MOTIL: Interferencepamma inducing factor; interferencepamma, killer rell: Interferencepamma andivinal agent; antimicrobial agent; humour; mYNEF: hepatitis; malaria; tuboroulosis; renal carolnoma; rissmantism; AlNS: asteograficals. Thrumbelsedia. acquired immunosed factory syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      whenestive ecities, hyperthyroidism, autorismnuce hepatitie, systemic solutistics, priymycellis, leukepenia, rhomacyjd archritis, HIV intections, asthma, atopic dermatitis, and pollinosis. The products may also be useful in the creatment of septic shock associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a murine interleukin 18 (10.15) polypopt to the line 18 is a type of cylothest to 19.25 transduction in immune systems. The interleukin 18 receptor polypopt do non be used to neutralise interleukin-18 activity or to treat interleukin-18 receptor susceptive diseases, especially to treat autolimente or allergic diseases or as an immunosuppressant. Conditions which may be treated include e.g. graft or organ rejection, permicious anaemia, insulin-related diabetes, discoid lupus crythematosus,
                                                                                                                WP1: 98-288747,26
N-ESDB: V32632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kurimoto M, Okura T, Toriqoe K; WPI; 98-469188/41.
                                                                                                                                                          (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Kurimoto M, Okamoto I, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference
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28-JUL-1997; JP-215488.
                                                                                                                                                                                                                                                                                                                   EP-845530-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W48968 standard; Peptide; 157 AA
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Local similarity 99.4%;
Les 156; conservation
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                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Best Logal
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Ep-861663.A2.
02-sep-1998.
04-FEB-1999. 301952.
25-FFB-1997. Tp.oss460
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                                                                                                                                                                                                                                                                                                                                     of e.g. hypertalcaemia, osteoclastoma, Behoet's syndrome, osteocarcoma, Statuta the matuld arthritis, deformity ostitis, primory hyperthyroidism and osteoprosis busclosure; page 34; 56pp; English.
Interleukin-18 (IL-18) or a functional equivalent can be used for Interleukin-18 (IL-18) or a functional equivalent can be used for inhibition of osteoclast formation IL-18 is used for treating or presention extendist related diseases = 9 hypercalcaemia, osteoclastoma Behoef's syndrome, stressarcoma, arthropathy chronic rheumatoid
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Mouse interleukin 18. II 18. osteoclast, hypotoalcaemia, osteopenia,
osteoclastoca Behoef's syndrome: osteosarouma: arthropathy: osteoporosis:
chronic pheumatoid arthritis: deformity ostitis; primary hyperthyroidism
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                                                                                                                                                                                                                                                                                                             arthritis, deformity estitis, primary hyperthyroidism, esteopenia and
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of interleuble 18 to
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                                                                                                                                                                                                                                                              157 AA;
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                                                                                                                                             99.4%:
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                                                                                                 Fred No. 1
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Fred. No. 2.9e-76;
0, Mismatches 1,
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                                                                                                             2.9e-76:
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                                                                                                                                                                                                                                                                                 Mutants of interferon-gamma inducing polypeptide usoful as antitumour, antiviral antimicrobial or anti-immunopathic agents PS Claim 6: page 44: 59pp: English.

Chaim 6: page 44: 59pp: English.

Chaim 6: page 44: 59pp: English.

Chair for present sequence represents the mutant mouse interferon-gamma or inducing factor midif/MUTI2. The wild-type mouse interferon-gamma or inducing factor and mouse interferon-gamma inducing factors in which one or more cysteine residues are replaced with different residues at or away or more cysteine residues are replaced with different residues at or away or more cysteine residues as hown in W4936 W49958. The mutant midiffs are obtained to be less texto, more active and stable interferon-gamma and are claimed to be less texto, more active and stable of interferon-gamma and are claimed to be useful as antitumour agents, antitumour formation, and may therefore be useful as antitumour agents, antitumour or immunotherapeutics, antitural agents and antimicrobial agents. But on mutant midiffs are also claimed to be useful for treating hepatitis.

Community dimmunodeficiency syndrome (AIDS), malaria, tubeliculais, solid on milignant tumours (e.g. renal carcinoma), theumatism, osteoporosis and thrombour process and chemo-therapy.
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Mutant mouse interferon-gamma inducing factor miolF/MUILZ.
Interferon-gamma inducing factor; interferon-gamma, killer cell;
antitumour agent; antiviral agent; antimicrobial agent; thusmar:sm. AIDS;
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15-SEF-1998
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Kurimoto M. Okamoto I. Yamamoto K;
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21-JAN-1997;
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28-NOV-1997;
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Misc_difference 125
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| Local Similarity
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                            NFGKLHT11AV18N1NI@VIFVIWF@PVFEDMIDID@SASEP@IFLI1YMX8DSEVEGLA -60
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VII.SVETSKMSTISCHWEITSCHEMERCHITT. CHITTELLE LEVYCHOMMSEESSCHEG 120
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                                                                                                                                                                                                                                                                      157 AA;
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"onservative
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Pred. No. 3.7e-76;
C. M.Smatches 1
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HIT ASSETTDATELTLENKERHODESVMETLINLESS

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Charles B, 155 TH
WITE 18 - 1.45 ZZZZZ
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Mouse interleakin 18. H. 18. Ostroclast, hypercalcaemia: ostropenia;
Mouse interleakin 18. H. 18. Ostroclast, hypercalcaemia; ostropenia;
Mouse interleakin 18. Ostroclast, hypercalcaemia; ostropenia; 
tation(ta) present and a hard
tation(s) research a mammal
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(ii) 18 (II, 18) or a functional equivalent can be used for

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AVTESVKDGEMSTESCKNKIISFE---

120 GHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS 157

60 AVILSVKUSKMSILSCKNKIISEEEMDEPENIUUIQSDLIFFQKBVPGHNKMEFESSIYE 119

1 NEGELHOTTAVIBNINGQVLEVGKEQ-PVEFEMTETEQSASEPQTELTTYMYKDSEVRGL 5-4

HEGELHOTTAVIESING VLEVEKEMER VILLMELIDETANLSQIFLI I MYKOSEVKGL 90

Matches 126;

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    Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                             quantitating stress in a mammal Claim 6: Page 33: 47pp. English.

This is the amino acid sequence of the rat interferon-gamma inducion factor (IGIF) isoform, also known as interleukin-18-alpha (II-18-alpha). It can be used to transform a cell, which upon its expression can cause the cell to produce rat IATF, i.e. IL-18 or IL-18 alpha. It is made by the deletion of 57 bases (860-417) from V20875, a probable exp. The antibody to IGIF Jond probes derived from it, are useful for detection of II-18 or II-18 alpha process.
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                                                                                                                                                                           can be used to quantitate stress in a mammal. Sequence 175 AA;
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Conti B, Joh TH;
WPT; 98-193622/17.
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08-SEP-1997; U15891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon damma inducing factors and related DNA - useful for
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77.7%: Score 631; DB 1; Lenath 175; 79.7%; Pred. No. 2.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5%
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64.88, Score 526, DB 1, I
Best Local Similarity 65.68, Pred. No. 1.7e-47;
Matches 101: Conservative D7, Mismatches 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor sequence is shown in W4899. The invention provides for mutant human and mouse interferon-gamma inducing factors (IGIE) in which one or more cysteine residues are replaced with different residues at or away from the consensus sequences shown in W48956-W4898. The mutant IGIEs are capable of stimulating immunocompetent cells for the production of interferon-gamma and are claimed to be less toxic, more active and stable than the corresponding wild type interferon-gamma inducing factor. The mutant IGIEs are also claimed to enhance killer cell cytotaxicity and/or induce killer cell formation, and may therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be useful as antitumous agents, antitumous immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGIFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malarja, thermatism, usteoporosis and thrombopenia caused by radiation—and chemo-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutants of interferon-damma inducing polypeptide - useful as antitumour articizal antimerobial or anti immunopathic agents claim 5: page 41: 59pc.

Their present sequence represents the mutant human interferon-gamma inducing factor [GIF/MUI21]. The wild-type human interferon-gamma factor sequence is shown in W48959. The invention provides for mutants of the sequence is shown in W48959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eccation/Qualifiers
Misc_difference 38
/note= "changed from dys in wild-type to Ser in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant human interferon gamma inducing factor IGIF/MUT21. Interferon gamma inducing factor, interferon gamma, killer cell, artitiment agent, antimizal agent; antimizal agent tumour; IGIF; hepatitis; malaria, tuberculosis, renal carcinoma; rheumatism; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W48962 standard: Peptide; 157 AA.
W48962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kurimoto M. Okamoto I, Yamamoto K:
WPI: 98-288747/26.
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03-JUN-1998.
29-NOV-1997: 309692
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29-NOV-1996: JP-333037.
21-JAN-1997: JP-020906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoperesis, thrembopenia, acquired immunodeficiency syndrome.
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                                                                                                                                                  120 GHELACCKEDDAFKLILKKKDENGDKSVMFTLTN 153
                                                                                                                                                                                              50 VT15VESEKISTLSGENKIISEKEMNPPENIKDIKSDIIFFQRSVPGHDNKMQFESSSYE 121
                                                                                                                                                                                                                                    51 VILSVKISKMSTISCKNKTISEEEMDEPENIDDIGSDLIFFQKRYPGH-NKMEFESSLYE 119
                                                                                                                                                                                                                                                                                  2 FORTESKUSVIANLNOGVERIOGONAFIJABUMIOSOSKUNAFETIFIISMYKDSQPRGMA 61
                                                                                                                                                                                                                                                                                                                               2 FGRLHCITAVIRNINDQVLFVDK-RQPVFEDMIDIDQSASEPQIRLIIYMYKDSEVRGLA 60
                                                                                                    GYPLACEKERDLEKLILKKEDELGDRSIMFIVON 155
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                    June 22, 1999, 10:56:40
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1.966 Million cell updates/sec
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Mutant mouse inter
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Interferon gamma i
Interferon gamma i
IFN gamma inducing
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Human interleukin
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Amino acid sequer
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Amino acid seguenc
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RESULT
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R92506
                                                                                                                                                                                                                                                                                                                                                                                                                         TOXXXUU>::
                                                                                                                                                                                                                                                                                                                                                                                                                 Protein that induces gamma interferon product in immunocompetent process: used e.g. as antiviral or antitumour agent, also induces provide the liver cells. The protein terferon gamma (Fryamma) inducer protein CC of the invention. This protein induces IFNyamma production in CC immunocompetent cells. The protein is useful as an antiviral, antitumour, antitumour, antitumour protein is useful as an antiviral, or it can be used in a preventing AIDS, condyound aduminatum, or it can be used in the protein can also be used to induce IFNyamma production in CC altery The protein can also be used to induce IFNyamma production in CC cultured cells. The Higherma induces fungishes the protein can also be used to induce IFNyamma production in CC cultured cells. The Higherma induces forced to induce IFNyamma production in CC cultured cells and when ised with intelleuking (IL-2) and timbur adaptive the protein unious. The DNA enoughed the effects of adaptive immunotherapy in tumours. The DNA enoughed the effect can using monocloud antibodies.
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                          Matches
                                  29-SEP-1996 (first entry)
Human interferce gamma inducer protein.
Interferce-gamma inducer protein: IFN-gamma: antimiral: wirucide:
Antilumous, antikacturial. immunotegulator: adoptive immunotherap
therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon gamma production inducer protein.
Interferon gamma, inducer, Invamma, inmuncapetent cell, antivital:
antitumour; antiseptic; immunoregulatory; platelet increasing agent;
therapy, preventice, analytem scuminatum, renal cancer, hash cancer;
grantism; myosis fundades; rheumatism, altergy, cytthe.alty, AIDS;
killer ("ell, interferi, int.", I.C. turbur nerrosis fartor; TNF;
adoptive immunotherapy; monoclonal antibody.
Komo sapiens.
                                                                                                                                                 E99564 Standard, Erntein: 157 AA
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Kohno K. Kunikata T. Kurimoto M. Okamura H.
Tanimoto T. Torigoe K:
WPI: 96-070177/08.
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13-JUL-1995; 304906.
14-JUL-1994; JP-184162.
10-FEB-1995; JP-045057.
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02-SEP-1996 (first entry)
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                                                                                                                                R99564;
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                                                                                                                                                                                                                                               16 NDOVLF 21
                                                                                                                                                                                                                                                                                    1 NDQVLF 6
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6; Conservative 0; Mismatche
Location/Qualifiers
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Fig. la s
fig. ruck
WPT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARSON BUT PROPERTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homas materia
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The mplical total total cells feron MKF was allowed produced recombinant total cells of the ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAYE) BEA
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                                                                                                                                                                                              A estodo a interferent damma prodn. inducina polypeptide
Tieut e i pro-ente e.g. viral disease, malignancies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z Z
Ž Ž
                                 : i : He 48 - 48pp
h: E: pr *oir
OY Smun : Smpot
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                                                                                                                                                                                                                                                                             Third is a second of the factor K. Without St. Kunikata I. Kunimoto M. Kara and the K. Withouto St. Tennology I. Tennology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i interest or a visual disease, malignancies and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lately low-ow, pred No. 2.5; Length 157; lately low-ow, pred No. 2.5; bit servation of Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - interferon-namma inducer protein.
- some later pastein, HTM gamma, antiviral, virueide,
- interferial: immunoregulator; adoptive immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ($1100 ts: 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Socal fon/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            impotent cells. It enhances the cy
r induces 'be formation of killer
                                                                                                               4 App: English.
                                                                  (R99558) induces intertered gamma (IEN-damma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ile. Thr
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                                     It enhances the cytotoxicity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "shio s:
                                                                                                                                                                                                                                                                                                                                                                                            Okamura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamura H;
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    useful
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R99560 ID R9 AC R9 DT 29

R99560; 29 SEP 1996 (first entry)

R99560 standard; Protein; 193

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                                                                                  Query Match
Best Local :
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Best Local Similarity
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1965; 308055.

15-NOV-1994; JP-304203.

23-FEB-1995; JP-058240.

10-MAR-1995; JP-078357.

18-SEP-1995; JP-262062.

29-SEP-1995; JP-274988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-712931-A2.
22-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic Treells). Recombinant IFN-gamma inducer protein can be produced high yields using host cells, esp. Escherichia cell; transformed with a vector carrying the encoding cNNA (7324-2). It is useful as an antiviral, antitumer, antibacterial, immanoremulatory and blood platelet enhancing agent, and can be used in adoptive immunotherapy. It is also used to raise monoclanal antibodies. A full image to sequence 157 AA:
                                                                                                                                                                                        Example A 3-2; Page 36-37, 48pp, English.

A novel mouse protein (P99550) induces interferon-gamma (IFN-gamma) prodn. by immunocompetent cells. Its sequence was deduced from that of a cDNA clone (T32403) isolated from a mouse liver library.

Recombinant IFN gamma inducer protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse mature interferon-gamma inducer protein.
Interferou-gamma inducer protein; IFN-gamma; antiviral; virucide; antitumour; antibacterial; immunorequiator; adoptivo immunorequiator.
                                                                                                                                                                                                                                                                                                                 {\bf DNA} establing in the first games producing polypoptide to treat and prevent, e.g. viral disease, malianancies and
                                                                                                                                                                                                                                                                                                                                                                          Tan.guchi M, Tanimoto T, Torigoe K, WPI: 96-252837/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R99559 standard; Protein; 157 AA.
                                                                                                                                                                           carrying the cDNA
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T32403
                                                                                                                                                                                                                                                                                                                                                                                                            (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Fukuda S, Kohno K, Kunikata T, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1996 (first entry)
                                                                  Local Similarity
16 NDQVLF 21
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                                1 NDQVLF 6
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                                                                                                                                                        157 AA:
                                                                100.0%; Score 31: DB 1; Lonath 157: ilarity 100.0%; Pred. No. 2.5; Conservative 0, Mismatches 0: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             Kurimoto M,
                                                                                                                                                                                                                                                                                                                                                                                         Ushio S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Slopui :
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Querr Match
Best Local
Matches
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15-NOV-1996; JP-354203.

23-FEB-1995; JP-958257.

16-MAR-1995; JP-978357.

18-SEP-1995; JP-262062.

29-SEP-1995; JP-274988.

(HAYB ) HAYASHIRARA SEIBUTSU KAGAKU.
FAARAB ; Kobar K, Kurikata T, Kuris
FAARAC K, Tanimoto T, Torigon K, T
                                                        J09157180-A.
17-J0911997.
24-JNN-1997. C28722.
04-GCT-1995. JP-279906.
10-MAR-1995. JF-37837.
29-879-1988. TR-274980
  (HAYR )
WPI: 97-
N-PSDB;
A drug (
                                                                                                                                                                                     W34362)
15-037-1997 (first entry)
Marine grotein for induction of interferon-gamma.
Interferon-gamma; immunocompetent cell; malignant tumour;
"'''' A'sease, bacterial infection; immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The matter outline of a momel began protein (P00560) induces interferon damma (IEV damma) prode, by immunocompotent cells. It is the ground if a DNA blone (I32.04) obtal from a human liver library. The protein enhances the cytotoxicity of killer cells and/or indices the formation of killer cells (e.g. NK cells, and/or indices the formation of killer cells (e.g. NK cells, and/or indices the formation of killer delis and cytotoxic T-cells) immunotable as an antivital induced a superficial inducery and blood platelet combancing agent and can be used in adoptive immunotherapy. It is also accept that is an accounted to a continuous continuous acceptable in acceptable in acceptable in a combancing agent and continuous acceptable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITT STB.
                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                           WD4DCD standard, Sriteli. WD4D5D:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding interferon gamma prodm. inducing polypoptide to treat and prevent, e.u. viral disease, mailgnancies and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human interferor gamma inducer profein.
Interferor Jamma inducer protein, IFN-gamma, antivixal, viruside,
antitumour: antibanterial immunicadulator: adoptive immunicherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
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                                                                                                                                                           _difference
                 97-369391/34.
DB: T80210.
                                            ) HATASHIRAFA SPIRHTSH KAGAKH
containing a pelypeptide which induces interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA,
                                                                                                                                                           Location/Qualifiers
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                                                                                                                                              /note=
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37. ...
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Prod. No. 3.2;
Mismatches
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K. Tishio S:
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RESOUT
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WL4L58
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Best Local S
Matches 6
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Hest Local Similarity 100.0%;
Matches 6; Conservative 0
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27-JCN-1097.
24-JCN-1095; C287L2.
24-JCN-1995; JF-279905.
10-MAK-1995; JF-27998.
29-SER 1995; JF-27998.
(HAYE) PAYASHIDARA SEIBUTSU KAGAKU.
WP1: 97-369391/34.
N-PSDB: T80209.
                                                          Homo sapiens.
                                                                           15-JAN-1998 (first entry)
Interferon gamma inducing factor-2 (IGIE-2) R1401 variant.
Interferon gamma inducing factor 2, IGIE-2, leccoyte, lynghisyts, hum
Interferon gamma inducing factor 2, IGIE-2, leccoyte, lynghisyts, hum
Inflammation; proliferation; differentiation; materation, blambe damus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production in immunocompetent cells. This protein may be used as the major represent in a drug for the piecetic may be used as the major represent in a drug for the piecetic and iterated of e.g. malignant tumours, wiral diseases, bacterial infections and immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein for induction of interferon-gamma.
Interferon-gamma, immunocompetent cell; malignant 'umcur:
viral disease, bacterial infection, immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Page 10:11, 12pp, Japanose.
This sequence represents a protein which induces interiestal gamma production in immunocompetent cells. This protein may be used as the major component in a dray for the prevention and theatment of e.g. malignant tumours, viral diseases, bacterial infertions and
                                                                                                                                                                                                                    W31757 standard; Protein; 193
W31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A drug containing a polypeptide which induces interferon pamma useful (or treating era, mallynunt tumours, viral, bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune diseases. Sequence 157 F
   Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1. Page 9, 12pp; Tapanese
This sequence represents a prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treating \alpha \gamma -malignant tumpurs, viral, bacterial or induce diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-00T-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 100.0%,
Local Similarity 100.0%;
hes 6; Conservative 0;
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      Location/Qualifiers
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Fred. No. 2.5;
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김댓글 걸고 동목으로 무무를 공성증 중중부터
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This proble sequence represents an interferon gamma inducing factor-2 (188-2) for the Sequence at iver cDNA library. This sequence divers it as 1815 2 (dontified from a T-lymphocyte cDNA library (W22047). A fact there is 1814 is found to be changed from Arg to Ile. A second right and the sequence of the second sequence is a sequence in the second representation of IGF-2 in conditions have a second with interest of with a recursion of a second representation of the second representation of the second representation of the second representation of the second representation of activity. The profession seed to discusse, prevent or treat IGF-2 induction is possible to the second representation of factor of the second representation of t
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                                 Is it is the beautiful separate of the reconstruction denimal inducing factor-2 of 2). We see a satisfie (W1204), and as IGH variant (W1204), and as IGH variant (W1204), and wist probes derived from the less than the used to quantify the expression of the second of the inflammation or aberrant resistors that the issociated with inflammation or aberrant resistors that it is also as an induced to screen for compounds tentered with IGH Lesson as an indices, antagonists or other tentered with IGH Lesson as an indices, antagonists or other tentered with IGH Lesson as an indices, antagonists or other tentered contains the problem of t
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"Spritally filosymes or antisense sequences) of IGIF-2
contribution the protein can also be used to diagnose, prevent
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Problems and as antimicrobial agent etc.

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Combisciosure, Page 22; 26pp; English.

Combisciosure; Page 22; 26pp; English
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Thehes 6; Conservative
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25-SEP-1996; 305997.
20-SEP-1996; JF-259105.
26-SEP-1995; JP-270725.
29-FEB-1996; JP-057434.
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Interferon gamma. IFN gamma; activital antionmotim: radiotherapy:
imbolomotive additional apent: whometherapy: werkepacita;
thrombocytopachia; immunocompotent cell; asthmu; huytovor;
rheumatism; interleukin; killer cell.
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Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto I:
WPI: 97-205381/19.
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26 - JAN - 1998
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16 NDOVLE
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09-APR-1997
26-SEP-1995: 305997
26-SEP-1995: TP-269105
26-SEP-1995: TP-27925
29-FEB-1996: UP-07025
(FAYE-) HAYFSHIBAPA SHIE
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W15701;
26 Jan 19.0
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Interferon-gamma inducer protein.
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tumours and as untimicrobial agent etc.
Claim 3: Page 19: 25pp: English
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    tumours and as antimicrobial agent
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JA.K. Eujli M. Kulimoto M. Nekada Y. Tanimoto T.
97-205381/19.
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Interference by a systil for additive laments.
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פי (המלים) PR 1: Length 50;
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Industino, antibody, dispositic assays fusion process a
WP1: 98-018522702.

N-PSDB: V05368.
Antuarchit if himse interlection: gamma from this is a large exceed by human Disclosure; Pages 54-55; 63pp; English.
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20.MAY-1396- US-66-998.
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Best Local Similarity
                                                                                                                                                                                                                                             This polypeptide induces IFN yamma production in imministropy tent relis (the polypeptide is not named but is described in the 277a/7a and 193785-78.) An engine in the release the presents form of this polyperide into this active form by cleaving a linkage between Asp at amino acid positive 18 and Tyr at amino acid position 37 at the precursor. The compute can be obtained from a human hasmatopelete relia and can be inhibited by independed and acetyl-fityresyl-fivelyl-fitalanyl-fit aspartified. The engine can be used for cleaving a recombinant HN-damen propolypeptide to form a mature polypeptide.
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18-JUL-1997: 305377.
30-MAY-1997: JP-156062.
19-JUL-1996: JP-207691.
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Claim 20: Page 17: 18pp; English.
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PESULT 3 WMYZ14 14K cell fusion protein - Vaccinia virus C:Species: vaccinia virus C:Date, 31-Mar:1939 #sequence_tests.cc /1-Mar:1949	Uy 1 NEGYLE 6 	Query Match Best Local Similarity 83.3%, Fred. No. 3.5; Matches 3; Consumutate 1, K.emarches	RESULT 2 G64005 hypothetical protein Hids04 Haumophilus Inflorate Cyspecies: Haemophilus Infloredae Cyspecies: Haemophilus Assertion: Hamas Mills Mills Infloredae Cyspecies: Cystem J. Scott, J. Schilor, F. Hill J. Scotty J. Schilor, F. Hill J. J. Schilors: Communication and the Arabidos Cyspecial Cyspe	Qy i NDQVLF 6 11 Db 51 NDQVLF 56	Query Match 100.0%; Score 31; DB 2; Best Local Similarity 100.0%; Fred. No. 2.1; Matches 6; Conservativo 0; Mismatches	Nature 378, 88-91, 1995 A,Title! Clouing of a new optobless that induses IFN: A;Reference number: Souzzó A;Accession: Souzzó A;Status: preliminary A;Molecule type: mRNA A;Pesidnes: 1-102 < OKAS A;Cross::Gletteles. EMELLELEGG MIT gl7945 FII	SULT 1 9226 tokine IGIF - mouse Species: Mus musculus (house mouse) Species: 10-Apr-1996 #sequence_rcvision 19-Apr-1996 Accession: Sbu226 Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M	ALIGNMENTS	40 20 83.9 201 2 395655 41 25 83.9 110 2 395655 42 25 83.9 110 2 750651 43 25 83.9 110 2 750154 44 25 83.9 422 2 764651 45 25 83.9 252 2 764651
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Virology 178, gt. 41, 1990
A:Tartor VarGit Francis induces cell fusion at acid pH and this activity is modiated by
Aukylakegor number: A 1976, MSID:MSS7795
                                                                                    Record, S. La.
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A: buten's an Matien possible protein-coding frames A:N Metablisher unincluded nor nucleation sequence is given Casupertamity: Therefold virus 14K cell fusion protein
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Alexander bettal sources strain Ceposhaqen
behadel S.J. Sohren, Gri Perkus, M.F. Davis, S.W.: Winslow, J.P., Paoletti, E.
Alexander 199, 17 Med. 1980
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All 19 Appet 1.4 for the complete DNA sequence of vaccinia virus".
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Addition Mapping and intelection sequence of the vaccinia virus denothat encedes a 14-ki
Additioning context A27173; MUID:88036210
Address, on: 621173
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J. Virol, 61,
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Best Local Similarity
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R:Moyle, M.; Napier, M.A.; McLean, J.W.
J. Biol. Chem. 266, 19650-19658, 1991
A:Title: Cloning and expression of a divergent integrin subunit beta-8.
A:Reference number: A41029; MUID:92011767
A:Accession: A41029.
G:Superiamily: integrin beta chain
G:Keywords: cell adhosion: cytoskoletca; duplication, extrabellular matrix: d:ycoprot
                                                                                                                                                                        A:Cross-references GR:M73780; NID-g194520, Ptp-g184521
                                                                                                                                                                                                                                                                                      A: Molecule type: mRNA
A: Residues: 1-760 /MOY>
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C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #rext_change ฟีซ์ Sep-1997
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C:Superfamily: yeast cytosolic phenylalanine--tRNA liquse alpha chain
C:Keywords: aminoacy1-tRNA synthetaso: ligase: protein biosynthesis
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A:Authors: Berondowsby, M.; Klenk, H.F., Flaser, C.M.; Smith, H.C., Woese, A.E.
A.Title: Complete genome sequence of the methanogenic archaeon, Methanocorous
A:Reference number: A64300: MMTD:06337999
A:Accession: C64438
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
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A:Residues: 1-548 /BUL>
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A:Moslidnes : MBL:M37086; NID:g335300; PID:g435301
A:Moslidnes : BMBL:M37086; NID:g335300; PID:g435301
C:Superfamily: vaccinia virus 14K cell fusion protein
C:Korwords : glycoprotein; membrane fusion
Fi2-136/Product: 14K cell fusion protein: #status predicted <MATS
Fi2-136/Product: 14K cell fusion protein: #status predicted <MATS
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On 3%. Score 28; DB 2, ixmath 548;
Best Local Similarity 83.3%; pred. NO. 37;
Matches 5: Conservative 1; Mismatches 6: Indoes
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Best Local Similarity 83.3%;
Matches 5: Conservative
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Score 28; Pred. No.

DB 2;

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hypothetical protoin 5 - vaccinia virus
C:Species: vaccinia virus
C:Date. 20-Feb-1991 =sequencironision 20-Feb-1995 #text_change 08-Sep-1997
C:Date. 20-Feb-1991 = Sequencironision 20-Feb-1995 #text_change 08-Sep-1997
C:Accession: S29911
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A:Cluss references, EMBL.X57318, NID:g60079; PTD:g60044
C:Superfamily, vaccinta virus 14K cell fusion protein
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A. M. Proble tire, DNA
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A:Accession: $29911
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                                fusion plotein, 14K · monkeypox virus
C:Species: monkeypox virus
C:Species: monkeypox virus
C:Jan: 36-Jan:1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Jaccession: S37281
C:Accession: S37281
R:Meyer, H : Csterrieder, x.v.z.: Czerny, X.V.7
R:Meyer, H : Csterrieder, x.v.z.: Czerny, X.V.7
R:Meyer, H : Csterrieder, x.v.z.: Czerny, X.Y.7
R:Meyer, H : Csterrieder, X.Y.Z.: Czerny, X.Y.7
R:Meyer, H : C
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A:Note: the source is designated as mousepex virus
C:Superfamily: "accinia virus 14K cell fusion protein
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A; Residues: 1:110 < MEY >
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A;Molecule type: DNA
A,Residues: 1 110 <MEY>
A;Cross-references EMBL X75155; NID;g404278; DID;g404279
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A;Accession: S37275
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C:Species: 06:Jun-1935 #Sequence_rects: doi:r:Jun-1935 #tewt_ctarge (9:Sep-1007
C:Accession: 837275
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C:Superfamily: Vaccinia virus 14% cell fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, September 1993
A:Description: identification of binding sites for neutralizing mabs.
A:Reference number: $37274
A:Arcession: $37274
A:Status: preliminary
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probable membrane protein budos - Escherichia cull
C:Species: Escherichia coli
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Best Local Similarity
Thomas 5; Conserv
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C:Cate: 06 Jun 1997 #s--pressor_position 06 Jun-1995 #fost, change 08-Sep-1997
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Andersonal Type INA
Andersonal 90, 64 (88)
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"Station 1 Nov 1965 Escapuace prevision 1 MCC 1965 #LCXL_chaide 20-Mar-1998

"Adversation of Late Journal, Station Station

E.France "M. "Secapuace T.D.: White, O.: Adams, M.D.: Clayton, R.A.: Eleischmann, R.D.:

M.: Ferrance "M. "Secapuace T.D.: White, O.: Adams, M.D.: Clayton, R.A.: Merrick, J.

M.: Ferrance "M. "Secapuace T.D.: White, O.: Adams, M.D.: Clayton, R.A.: Merrick, J.
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A:EXP-13 outal and on strain K-12, substrain MG1655
TiBergands: Et undweebtado protein
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Reperties F. R. D. Okett Hill G.: Bloch, C.A.: Perna, N.T.: Burland, V.: Riley, M.: Co.
A. Resea D.: Mill. B.: Shau, Y.
A. B. Stenow, 27, 1154 (14) 2, 1997
A. D. Bertand, 17, 1154 (14) 2, 1997
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A:Cross-references: EMBL:X17617: NID:g65470; FID:g55473
C:Keywords: DNA binding: transcription regulation: zinc finder
                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Title: A mouse zinc finger gene which is transiently expressed during spermatewenes A:Reference number: $07667; MTID:90107944
A:Accession: $07667
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A:Cross-references: GB:J04770
R:Cunliffe, V.; Koopman, P.; McLaren, A.: Trowsdale, J.
EMBO J. 9, 197-205, 1990
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C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change (0.Sep-1997)
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RESULT
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Best Local Similarity
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Matches 5: Conservative
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MEDILINE: 97186574.

BLACK PA. PAUCH C.T. KCZLOSKY G.J. PESCHON 7.1. SLACE J.I.

BLACK PA. A. PAUCH C.T. KCZLOSKY G.J. PESCHON 7.1. SERNE J.I.

MOLESON M F CASTNEP B.J. STOCKING K.L. KEDDY F. SRINIVASAN S

MITISNES J.N. JOHNSAN F.S. FAXILAR K... MAKCH L.J. GERRETI D.E.

TA metalloproteinase disintegrin that releases tumour-necrosis

factor alpha from cells.":

MATURE 385:729-738(1997).

EMBL: U69611: G1858022: -.

EMBL: U69622: G2039383: -.

EMBL: U69602. G2039383: -.
                                                                                                              01-JAN-1998 (TFEMBLPEL 05, 01-JAN-1998 (TFEMBLPEL 05, 05, 01-AUG-1998 (TREMBLREL 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MERSTER A., BUTLER M., KNIGHT G.C., AMOUR A., SLOCOMRE P.M., WERSTER A., BUTLER M., KNAYDER V., SMITH B.I., STEPHENS P.E., SHELLEY C., HUTTON M., KNAYDER V., DOCHERTY A.I.P., MURPHY G.:
"The TNF-alpha converting enzyme ADAM-17 is inhibited by line subkitter (TTL-1999) TO FMBL STENBAME, TOTAL ZALA FAMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EURAPYOTA: METAZOA: CHOPPATA: VERTEBBATA: MAMMALTA: EUTHEBTA:
PODENTIA: SCIUROGNATHI: MUPIDAE: MUPINAE: MUS.
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ARCHAEA: EURYARCHAEOTA: METHANGBACTERIALES; METHANGBACTERIACEAE
                              METHANOBACTERIUM THERMONUTOTROPHICUM
                                                                                         SENSORY
                                                                                                                                                                                                                                      027196
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827 AA:
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Fred. No. 84;
1, Mismatches
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TNF ALPHA CONVENTING ENZYME (FACE)
: C9DEA655 CEC32:
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Q230TR
Q1 VV 12996 (TREMBLEEL Q1 ...
Q1 VV 1000 (TREMBLEEL Q2 ...
Q1 VV 1000 (TREMBLEEL Q8 ...
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BYST W. CONNET M. CORSEY T. CORFER J. COLLSON A. CRAXTIN M.
DEAR S., DC Z. LUMBEN F. FAVELLO A. FULLTON I. GARRINGE A., GREEN F
HAWKINS T. HILLIEF I. JIEF M., SCHNSTON I., CONES M., KLESHAW J.,
KIPSIEN IAISEER N. IATREILLE P., LIGHTNING T., LLOYD C.,
KIPSIEN T. HOLLIEF I. O'CALLAGHAN M., PARSONS J., PEPCY C.,
FISKEY: F. CEA A. SAUNDES S. O'CALLAGHAN M., PARSONS J., PEPCY C.,
FISKEY: F. CEA A. SAUNDES S. SHOWNER F., SMALLON N. SXITH A.
SONNHAMMER E., SIADEN N. SULSTON J., THERRY-MIEG J., THOMAS K.,
VAUGIN M. VAUGHAN K. WAIEFSTON F. WAISON A., WEINSTOCK L.,
WILKINSON-SPECAL J., WOBLDMAN P.,
WILKINSON-SPECAL J., WOBLDMAN P.,
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EUKARYOTA: METAZ: A: NEMATODA: SECERNENTEA: RHARCITIA: RHABDITIDA:
EUKARYOTA: WETAZ: A: NEMATODA: SECERNENTEA: RHARCITISA
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STRAIN=DEL
MEDITNE: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cumplete genome sequence of Methanobacterium thermoautotrophicum deltaB: functional analysis and comparative genomics "; J. BACTERIOL. 179:7135-7155(1997).

SEMBL: AEOCORRO: G2622227: -
SEQUENCE 348 AA: 3930 MW: G4ABABE6 GRC32;
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ALIDRETATE I RASHIFFARISH P RIAKETY D., COUR D.
HANGI I RAGGE P LIMM W. POTHTER B. QIU D.
HANGI I RAGGE P LIMM W. POTHTER B. QIU D.
SPACHAFORA P VITARE WANG Y MIEFZEOWSKI J., GIESON R., JIWANI
CARTS A BYTH SATURIL D. FRABHAKAR S., MIDOUGALL S
SHIMER G., GOVELA A PITT-OVEKI S. CHUPCH G M., DANIELS G J.
MACCI - I RICP P. NOTHING J., REEVE J.N.,
MACCI - I RICP P. NOTHING J., REEVE J.N.,
                                                                               STRAIN-BRISTOI N2.

WAIERSION R.:
SUBMITTED (JUL-1996) TO EMBL/SERBANK/LUBY LATA BANKS
EMBL: 064840; G1465791; -.
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elegans.":
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MEDIINE: 94150718
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COSMID 20317)
                                                                  SEQUENCE
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EMBL: U53141: G1255362) 1.
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SUBMITITE (ARRITAR) IT EMBL/BLURANK/LURC LAIA BANKS
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AND LAST W. BANKES C. BERKS M. BONFIELD J. CONTROL M. CRANLON M. CRANLON M. TRANSLER M. COULSON A. CRANCES A. GREEN P. CONTROL M. COULSON M. KERSHAW J. CANCELLE M. LIGHTNING J. LICYD C. M. SATHELLE M. LIGHTNING J. LICYD C. M. SATHELLE M. LIGHTNING J. LICYD C. M. SATHELLE M. C. SHEWNKEEN R. SMALDON N. SMITH A BANGEN S. LIGHGEN M. THILEFT MICH. THEMAS K. VALUAN K. WALESTEIN H. WATTON A. WEINSTOCK I.
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FUNYIES: SIEBMAT-PHYIA; MAGNOLIOPHYIA;
WELLTAPARALES: RPASSITACEAE; ARAKIDOPSIS.
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Thinks 5: Conservative
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ALIENSCHMIDT 0. BOKRANZ M., FUCHS G.:
"Novel actuble 2 aminobenzoate metabolism. Nucleotide sequence of
"Novel actuble 2 aminobenzoate metabolism. Nucleotide sequence of
plasmid carrying the gene for the flavoprotein 2-aminobenzoy)- "vA
monocoxygenasc/reductase in a denitrifying Pseudomonas sp.";
CUR. J. BIOCHEM. 2017.15-722(1992).
-1-SIMILARITY: 10 GENE 11 AND X PROTEINS (P154.9) FROM
BACTERIOPHAGE 12-2.
EMPL. MILICAL PROTEIN: PLASMID.
SECTENCE 372 AA. 42362 EM, 44330571 GRC32;
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61-JAN-1998 (TREMBUREL 05, LASI SEQUENCE OPDATE)
01-N-V-1998 (TREMBUREL 05, LASI ANNOTATION 05-00TE)
RESISTANCE COMPLEX PROTEIN 12C-2.
12C-2.
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01-NUV-1996 (TREMBLEEL 08, LASI SEQUENCE UPDATE)
01-NUV-1998 (TREMBLEEL 08, LASI ANNOTATION UPTATE)
HYPOTHELICAL 42.2 KD PROTEIN (ORF 5).
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PEAM: PE00931: NB-ARC: 1.
SECUENCE 1240 AA, 141523 MW: 15E39309 CRC3.:
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The 12C family from the wilt discuse resistante locus the nucleotide binding, leucine-rich repeat superfamily
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EURAPPERS FOR ESCUTENTIAL (TOMATO).

TEACHEOPHYTA: VIPILIBLANIAE: SHAPOPHYTA: MARNOLIOPHYTA:

EURIPPERTA: ELPHYLLOPHYTES; SPERMATOPHYTA: MARNOLIOPHYTA:

EURIPPERTA: ELPHYLLOPHYTES; SULANNANAE: SULANALES: XULANACIDAT: SULANYTH

EURIPPERTA: XULANACIDAT: SULANNANAE: SULANALES: XULANACIDAT: SULANYTH
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PLASMID PKB740.
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EMBL AFOUAND; G2258317; -.
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Fred. No. 2.2e+02
l; Mismatches
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Pred. No. 58;
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MEDLINE: 92114475.

TONSSON R. SIGNAS G. MURIER H. P. LINEBERG M.:

TWO different grows arrows fibronavin binding proteins in Stephylamorous surface. The complete nucleotide sequence and characterization of the second gene.";

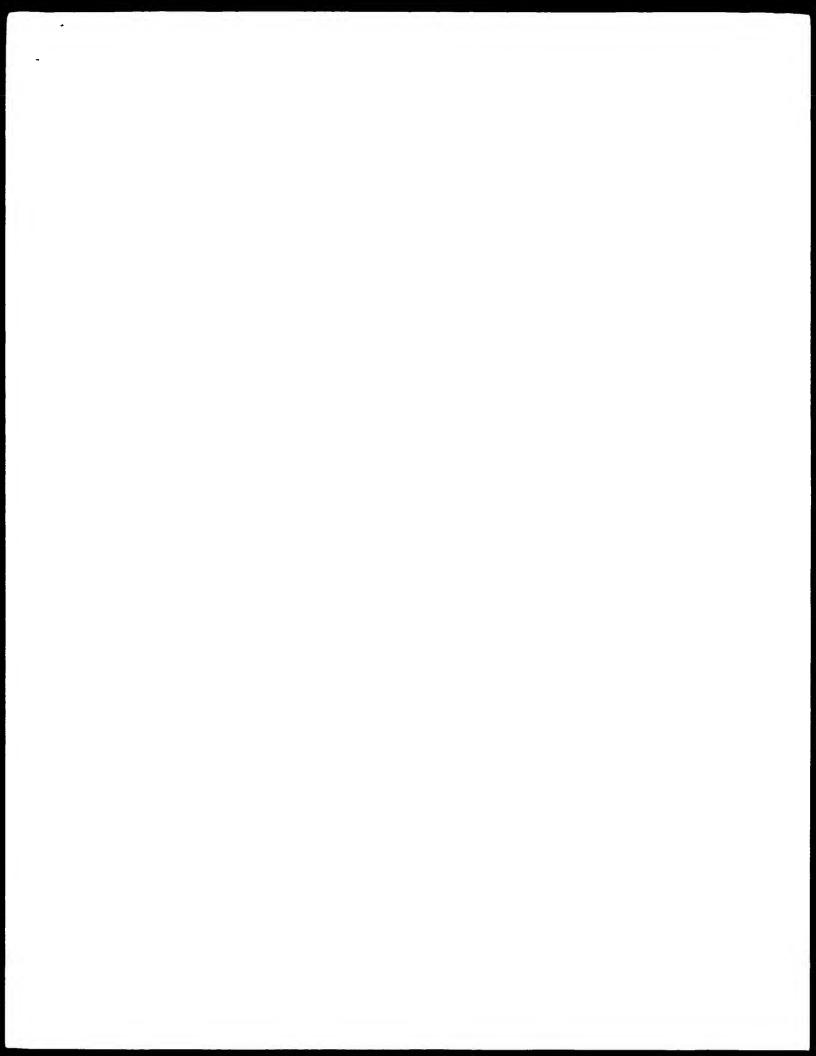
EVERT T. SIGNAS G. MURIER 1993.

EMBL. MEDICAL OFFICE T. SECOND (1993)

EMBL. MEDICAL GROWN DESABOSC OFCIA.

PERM. EPONIS G. STEPPS GROWN DESABOSC OFCIA.
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ENVELOPE PROTEIN.
NON_TER 1
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SEQUENCE 91 AA:
  01-NOV-1946 | 01-NOV-1946 | 01-NOV-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1946 | 04-1
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Q77573;
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Q53682;
Q1-NOV-1996 (TREMBLREL 01, CREATED)
Q1-NOV-1996 (TREMBLREL 01, LAST SECREMCE UPDATE)
Q1-NOV-1996 (TREMBLREL 08, LAST ANNOTATION UPDATE)
PTERCORECTIN BINDING PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUIKFN C., GOUDSMIT J.; SUBMITTED (JUL-)446) TO EMBL/GENHANK/DDBJ DATA BANKS EMBL: 276336; E254051. -.
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STRAIN-PATIENT MOTHER 566, 24-MONTH SAMPLE;
SIMONON A KAMPINGA G.A. VAN DE PEPPE P, KAPITA E., MSELLATI P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN IMMUNOSEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRUSES: FETEOID VIRUSES: FETEOVIRIDAE; LENTIVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL, 01, GREATED)
01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)
ENVELOPE PROTEIN (FRAGMENT).
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STRAIN-8325-4.
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BACTEBEA, FIRMICIES, BACTLUSATO STRIFFOM GROUP: BACTLLACEAE, STAPHTLOCOCCUS.
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83 98; Prod No 1 Koto2;
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1: Mismatches
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STRAIN-PATIENI CHILD 566, 24-MONTH SAMPLE;
SIMONON A , KAMPINGA G A , VAN DE PERBE P ,
                                                                                                                                                                                                               KILKEN O
                                                                                                                                                                                                                                                             HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1). VIRUSEE: FEIRUID VIRUSES: FEIRUVIRIDAE: LENTIVIRUS
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

June 22, 1999, 10:56:39; Search time 61.72 Seconds (without alignments) 2.294 Million cell updates/sec

Sequence Title: Perfect score: US-09-030-061-3

Scoring table: BLOSUM62

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standard. Flotein: 157 AA. 1996 (first entry) From gamma production inducer protein From gamma production inducer, protein From gamma production inducer, protein From gamma production inducer, protein From gamma producer, IFNgamma Landard, patelectionress; The protein inducer, inducer, protein From grossis flogoids, themsetier allers; protein From grossis flogoids, themsetier allers; protein From grossis flogoids, themsetier allers; protein From grossis flogoids, themsetiers From grossis flogoids, flogo	43- 4 (€) H
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WAY 1994, UP 49-8241.

WAY 1994, UP 278-86.

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A b --1 human protein (89954) induces interferon-gamma
(FN namma) product by immunocompetent cells is the product of a
(150 namma) product (T224]) derived from a human liver library.

FINA clone (T324]) derived from a human liver library.

FINA clone (T324]) derived from a human liver library.

FINA clone (T324]) he clone (T324) governorment of recombinant in the protein. This was used to construct hybridgem H-1, which are dereof until FN damma inducer protein monoplonal antibody H-Imah
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to true and precent, e.g. wirel disease, malignancies and immune
                                                                                                                                                                                                                                                                                                                                                                                                    NA Prico (S) interteron damma producing the tipe of the present, e.g. viral disease, male
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refus temma inducer protein; EPS-gamma; antiviral; virueide;
refus unlibactorial; immunorequiator; adoptive immunotherapy
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us perfects (R99558) induces interfection damma (

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7.1789, 4.
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for one from No. 2.3;
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                                                                   induces interfection damma (IEN damma) s It embaneos the cytotoxicity of
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                                     R99560
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                                                                                                                                                                                                Query Match
Best Local Similarity
Matching 2 Commont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1995: 308055.
15-NOV-1994: JP-304203.
23-FEB-1995: JP-058240.
10-MAR-1995: JP-078357.
18-SEP-1995: JP-262062.
29-SEP-1995: JP-274988.
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                                                                                                                                                                                                                                                                                                                                  Example A-3-2: Page 36-37: 48pp: English.

A novel mouse protein (K3955) induces interferon damma (ifferdamen) produced mouse protein (K3955). Its sequence was deduced from that of a cDNA clone (T3403) isolated from a mouse liver intrury. Recombinant IFN-gamma inducer protein can be produced in blab violate using host cells, esp. Escherichia coli, transformed with a vector using host cells, esp. Escherichia coli, transformed with a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuda S. Kohno K. Kunikata T. Kar
Taniquchi M. Tanimoto T. Toriqoe K.
WPI: 96-252927/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon-gamma inducer protein: IFN-quamma; antivital; viraction antilumour: antibacterial. Immunoregulator, adoptive industributory
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Mouse mature interferon-gamma inducer protoin.
R99560:
                R99560 Standard, Protein: 193 AA.
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                      carrying the cDNA.
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22-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding interferon gamma production bolypeptide cusefu-
to treat and prement, e.g. wiral disease, moliquancies and immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T32403
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Fukuda S, Kohno K, Kunikata T, Ku
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                                                                                                                     132 FKLILKK 138
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29-SEP-1996 (first entry)

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17-JUN-1997.
24-JAN-1996.
04-CGT-1995.
10-MAR-1995.
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The mattre posttlos of a nowel human protein (PAG56) indices interferon gamma (IFN-gamma) prodon, by immunocompetent cells. It is the product of a cDNA clone (T32404) obed from a human liver library. The protein enhances the cytotoxicity of killer cells and/or indices the formation of killer cells (e.g. NK cells, lymphokide-postivating killer (EAK) cells, and cytotoxic Techls). The mature protein (see also R9958) is useful as an antiviral, antifumor, antibacterial, immunoregulatory and blood platelet enhancing agent and can be used in adoptive immunotherapy. It is also used to raise monochonal antifundies
                                                               WPI; 9
N-PSDB: T80210. A drug containing a polypeptide which induces interferon-gamma \bar{A}
                                                                                                                                                                                                                                                                                                                                                                                        Murine protein for induction of interferon-gamma Interferen jamma immunecompotent cell, maligrant viral disease: bacterial infection; immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HAVE ) HAYASHIBARA SEIBUTSU KACAKU.
FUKUGA S. KONDOK, KUTUNTA T., FUKUMCTO M.
TADAKUJUCHI M., TAKIAOLO T., TUFIJUM K., UShio S.
WPI: 46-252007,05
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10-MAR-1995; JP-078357.
18-SEP-1995; JP-262062.
29-SEP-1995; JP-274988.
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22-MAY-1995.
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Interferon Jamha Induced protein, IEN-gamma; autiviral; vizucide;
antivemour, astibuctorial: immunorogulator; adoptivo immunocherapy;
thorapy; cancer.
                                                                                                                      20-200-100E.
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15-NOV-1994; JP-304203.
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                                  3) HAYĀSHĪBĀFĀ SĒTENTSN KARAKN
97-369391/34.
DB: TEC210.
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                                                                                                                   020722.
JP-279906.
JP-078357.
JP-274688
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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37. .193
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Pred. No. 2.8;
Mismatches of
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une disease.
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RESULT W31757 W31757 W3 DT 15 DE 17 DE 17 KW 15 
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Hest Local Similarity
Technical 7: Conserv
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Matches Terrory
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17-JUN 1997.
24 JAN 1995: 018711.
04-001-1995: JP-279906.
10-MAR-1995: JP-079357.
29-SEE-1995: JP-079387.
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WPI; 97-369391/
N-PSDB; T80209.
                                                   Homo sapiens.
                                                                                                                                                                                             W31757 standard: Protein: 193 W31757,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune diseases
Jaim. Taje 9. 12pp, Japanese.
This exquence represents a protein which induces interferon-gamma production is immunocompetent wells. This protein has be used as the major component in a drug fur the prevention and treatment of e.g. mailgoint tumours, viral diseases, bacterial infections and immune diseases.
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                                                                        Interferon gamma inducing factor 2 (IGIF-2) R1401 variant.
Interferon gamma inducing factor 2, IGIF-2, leacheyte, lymphocyte; hinfluorethin proliferation differentiation, materation tissue dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A drug containing a polypeptide which induces interior useful for treating e.g. malignant tumeurs, /iral, but
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Misc_difference 140
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Sequence 157 A
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9/-369391/34.
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130.0%;
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Pred. No. 2.3;
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in may be used as
and treatment of
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this is the present sequence of interferon damma inducing factor-2 (III 2). At 5011 2 variant (W21757) and an IGIF variant (W22049), which may be an alternate transcript, also exist, Probes derived from the 11e or a sequences can be used to quantify the expression of 5019 in scalifions that are associated with inflammation or aberrant expression of 5019 2. The protein can be used to screen for compounds that are represented as an atlandace, antagonists or other unitable of sequentially about most sense sequences) of IGIF-2 white to the protein can also be used to diagnose, presented to the control of the protein can also be used to diagnose, presented to the can be used to diagnose, presented to the control of the protein can also be used to diagnose, presented to the can be used to the can be used to diagnose, presented to the can be used to diagnose, presented to the can be used to the can be used to diagnose, presented to the can be used to the 
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3: <u>Б</u>
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it is a live at the fiff 2 sequence presented in W22047.
I clean
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                                                                                                                                                                                                                                                                                                                                                                                                          ite 45: 50pp; English.
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number addacted factor 2) MHF 2; leucocyte; lymphocyte;
4,5 j: Jiterations differentiation, materation, tissue damate.
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"Wild type Are is replaced by The"
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Query Match Hest local Similarity Tracks 7: Conserv

Conservative

180.001 0.

Score 33;

Condit 155

Mismatches

132 FKLILKK 138

1 FKLILKK 7

W15701

W15701 standard, protein, W15701;

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3
pisclosure) Page 22: 25pp. English.

Combined the present sequence represents a novel protein from mouse liver cells. The present sequence represents a novel production in immunecomporent cells. This pitter changes cytotoxicity of killer cells and indices of their formation. It is used as an automotic agent for antitumour financial cells in the treatment of atopic or immune system diseases, e.g. asthmatically in the treatment of atopic or immune system diseases, e.g. asthmatically and in the treatment of atopic or immune system diseases, e.g. asthmatically district including anti-Alicy or antitudent in the atopic or immune system diseases, e.g. asthmatically district indicates with intellection with such asthmatically of the protect system diseases. The immunesteraphy of leukaemia and other concers. When used the immunesteraphy this nevel protect associated with used the intellection of its of intellection to the patient (before affinity in protect to the patient (before affinity in patient) are being unown.
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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26-SEP-1996; 306997.
20-SEP-1996; JP-269105.
26-SEP-1995; JF-270725.
26-SEP-1995; JF-067434.
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Interferon-gamma, IFN-gamma, anti-interferon-gamma, anti-interferon-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or treat IGIF'S inductive of preliferation, differentiation or maturation of leadwaytes at lymphocytes, especially in relation to fissue damage associated with inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immuno:competent cells - useful for adoptive immuno:therapy of
tumours and as antimicrobial agent etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein that induces interferon-gamma produc
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a K., Fujii M., Kurimoto M., Nukada Y., Tastmoto I:
97-205381/19.
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Pred. No. 2.8:
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26-JAN 1998 (first entry)

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WASSOLI WASSOL
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Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                             #46592;
21-MAY-1998 (first entry)
Amier hid argumes of Liman isterleubis-legamma.
Interleubis-legamma, II-legamma; messe, cytekine, IGIE; isterferos-gamma.
Induction entitledy, diagnostic assay: fusion protoin, activity.
Immure-legical disorder, allergy
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Claim 8: Page 20: 26pp. English.
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AKIL: F. EJJIL M. KILIMOLL M. NJ
WPI: 67/205781/19
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Interferon-gamma, IPN-gamma, activital; antiongotic; radiotherapy; immunoregulatory, antitumour agont; chemotherapy; leukopaenia; thromboty openia, immunoremy obtains actima, hayfever, rheumatismo interleukin; killer cell
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26-SEF 1905 TF 276725
29-FER-1906: TP-067434
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20-SEP-1996; πρ-269
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Query Match
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27-JUN-1997: 304616.
27-JUN-1996: JP-186305.
27-JUN-1996: JP-186305.
(HAVB.) HAVASHIBADA SEIBUTSU K.
(HAVB.) HAVASHIBADA SEIBUTSU K.
KURIMOLO M. OKUTA T. TOXIQOO K.
WPI. HAVASASIA/UG.
N-FSCB: V15825, V15825.
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Razan IF,
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Interferen-gamma ITN-jampa, production inducer, gene ihrrapy/
immunosyspetent nell ihrettheath prevention, malignant tunour;
yiral infection; brototia, infection, immuno disease.
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W47429;
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Immunological disorders caused by human IL-1-gamma
Disologue: Pages 54-55; 63pp: English
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N-PSDB: V05368.
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This is an interferon damma (IFN-gamma) inducing polypeptide sequence. This really-edide induces (FN-gamma) reduction in immunocompetent cells (the polypeptide is not commed but is described in JP 27198/96 and 1.44-296. As a symmetric commed but is described in JP 27198/96 and 1.44-296. As a symmetric commed to be presented form of this polypeptide point this river form by closwing a linkage between Asp at amino acid position 47 of the precursor. The charge car is of intend thomat hormathy polypeptide cell and can be shown to be reduced to the precursor of the charge of the control and the polypeptide.
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interferc inducing polypoptic
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    1.5 feb. on the polypophido inducing infortoron-gamma effect by smmuno competent colls, useful to treat e.g. buman that theory or wital dispasses
    2: class 4 feb. 74pp. English.

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firms induction mattro polypeptide.
    firms (FN samma) precursor: enzyme; cleavage

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Best Local :
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                                                                                                                                                                                                                                                                                                             Polypeptide processing enzyme for preparing mature term of interferon inducing polypeptide claim 3: Page 15: 18pp: English.
This sequence represents the precursor of an interferon quanta (IEN-dumma) inducing polypeptide. The polypeptide induces IEN-damma production in inducing polypeptide. The polypeptide induces IEN-damma production in immunocompetent cells (the polypeptide is not named but is described in JP 27199,96 and 192090,96). An enzyme can convert this pre-cursor form into its active form by cleaving a linkage between Asp at amino acid position 36 and Tyr at amino acid position 37 and Tyr at amino acid position 38 and Tyr at amino acid position 39 and Tyr at amino acid position 30 and Tyr at amino acid position 30 and Tyr at amino acid position 30 and Tyr at amino acid can be enzyme can be estained from a human humantepolitic valyi in alamid separt 1 at. The enzyme can be used for clearing a recombinant IEN damino pro polypeptide to form a mature polypeptide.
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30-MAY-1997; JP-156062,
19-JUL-1995; JP-207691,
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Interferon-gamma, TEN-gamma, procursor, conymos cleavage.
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GenCore version 4.5

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Run on: Tune 22, 1999, 10:58:45 ; Search time 61.51 Seconds (without alignments)

4.263 Million cell updates/sec

Title: US-09-090-061-3
Perfect Score: 33
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A:Genome: plastid
C:Superfamily, DNA-directed ENA polymerase beta chain
C:Keywords: nucleotidy)transferase, plastid; transcri
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                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: "ucleic acid sequence not shown: translation tot
A:Molecule type: DNA
A:Residues: 1-1024 <WILD
A:Cross-references: EMBL:X95275; NID:g1171583; PID:c220243
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P:Iserentant, D.: Verachtert, H.
Yeast 11, 467-473, 1995
A:Title: Cloning and segmenting of
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A: Residues: 328-1024 (GAR)
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A:Accession: 872282
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J. Mol. Biol. 251, 155-172, 1996
A:Title: Complete gene map of the plastid-like DNA of the mularia purasite Plasmodism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-directed PNA polymerase (EC 2.7.7.6) beta ebain, plastid Flasmodium in CrSpecies: plastid Plasmodium falciparum  
OrDuto: 31:Decc1998 #scappense_revision 15:May 1998 #LoxL_chunge 26:May-1998  
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C:Keywords: oxidoreductase
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C:Species: Schwanniomyces occidentalis
C:Date: 27-Oct.1995 #sequence_revision 03-New-1995 #text_claute 09 Sep-1947
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Althogology (Chic. Typ. A. 1905) (Chic. Sequences. GB. 544184. NID. 3254433. PID. 3254934.

A) Note: Sequence extracted from NCBI backbone (NCBIN.112737, NCBIP.112738)

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A;Accession, $24772
A;Residues, lollid;,100:178,239,293 :HA2
B;Isq, N.H., Bertande T.M., Tsail, M.V., O'Malley, B.W.
J. Bill The Training T. 1972
A;Ille, Member T. The Statistic Ference superfamily interact.
A;Reference number: A43333 MHTD:40389108
A;Accession, A4333
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R:Blattner, F.R.: Plunkott III of Plock, C A Porns, N T. Burland, V. A.: Rose, D T. May E. Shao, Y. Siling 277, 1821-1822, 1927

A:Title: The complete genome 3-40-day of Escherichia coli K-12 A:Bosons of content Arabon 270, Arabons of Roses of Roses and Arabons of Roses of Roses and Roses of Roses and Roses of Roses of Roses.
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A Exference combact (F1764, MMTD 91342924
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C:Addession. 817554; S24672, A43397, A56407
R:Ha, I.: Lane, W.S.: Reinberg, D.
Nature 352, 689-695, 1991
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A;Residues, 1:316 KHAID
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A:Molecule type: mRNA
A. Residues. 1 208 WARN
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A:Cross references: EMBL::13654
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A:Title: Crystal structure of a TFIIB TBP TATA element termary complex.
A:Poference number: A57980
A:Contents, annotation, X ray crystallography, 2.7 angstroms, regidues 112-316
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B. 1942, Refer to Signal or quetre feature problemed of
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p:Hisatako K. Malik, S.: Poodor: 8.G.: Horikoshi. M.
Nucleid Adds Res. 13. 0533, 1391
A:Title: Conserved structural motifs between Xenopus and human
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C.Species. Xemopus laevis (African clawed frog)
C.Pator 20 Noveley (#sequence_remistre of hearlage #rext_change 17-Jul-1908
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A; Authors: Venter, J.C
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1.Species. Burrolla butydorferi (byme disease spirochete)
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probable membrane protein NJF1260 yeast (Saccharomyces cerevisiae)
N.Alternate names: hypochetical protein 12050
C:Species. Saccharomyces cerevisiae
C.Date. 20:Aug.1990 = sequence_revisiae
C.Accession: S57149
R:Rose. M.: Koetter. P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56848
A:Residues: 1-811 <ROS>
A:Residues: 1-811 <ROS>
A:Cross-references: EMEL:249626: NID.g1015854) PID:g1015855; MIPS:YJR126c
C:Genetics:
A:Map position: ICR
C:Keywords: transmembrane protein
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hypothetical protein slr1066 - Synechocystis sp. (Strain PCC 6803)

C.Species: Synechocystis sp.

C.Species: Synechocystis sp.

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Length 568;
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ER E., CONWAY A.B
LI Y., PALM C.J..
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C066122;
T C066122;
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T C1 NOV-1998 (TREMBLREL, 08, CREATED)
T C1 NOV-1998 (TREMBLEEL, 08, LAST SEQUENCE UPDATE)
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DT O1-NOV-1998 (TREMBLEEL, 08, LAST ANNOTATION UPDATE)
DE HYPOTHELICAL 30.1 KD PROTEIN.
OS BOPFFLIA BURGEOPPEPET (LYME DISEASE SPIROCHAELA).
OS BOPFFLIA BURGEOPPEPET (LYME DISEASE SPIROCHAELACE).
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Best Local Similarity
Traches 5: Conserv
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             EMBL: AJ222813; E1315191; -.
CHAIN 37 194
                                   STRAIN-SPRAGUE DAWLEY: TISSUE-WHOLE BRAIN; CULHANE A.C., HALL M.D., ROTHWELL N.J., LUHESHI H. "TLLILG OF rat brain interfeukin läckna.", MOL. PSYCH. 3:362-366(1998).
                                                                                                                                                                                        01-NOV-1998 (IREMBLREL 08, GREATED)
01-NOV-1998 (THEMBLREL 08, LAST SECUENCE UPDATE)
91-NOV-1998 (THEMBLREL 08, LAST ANNOTATION OPDATE)
                                                                                                                                                                                                                                         088749;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AKINS D.R.;
SUBMITTED (JUL-1998) TO EMBE/GENBANK/UDBJ DAIA BANKS
EMBE, U30617; G3309517; T.
HYPOTHETICAL PROTEIN.
SEQUENCE AT A AA. CUITA MW. BJC41581 DRC72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LI M., NORGARD M.V., PADOLE J.D.; "Evidence for in vivo but not in vitro expression of a Pointeila burdedorfer journe surface protein F (OspE) homologue."; MOC. MICROBIOL 18-507-520(1995).
 BUNBUURS
                                                                                                                        EUKARYOTA: METAZOA: CHORDATA: VERTERPATA: MAMMALIA: EUTHERIA:
RUFENTIA, COIDEUJNAIBI, MURIJAE, MURIMAE, RATTUS.
                                                                                                                                                  IL-18
RATTUS NORVEGICUS (RAT)
                                                                                             SEQUENCE FROM N.A
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 194 M.;
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 22313 MW;
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71.48;
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              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 9;
Pred. No. 47;
2; Mismatches
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i: Mismatches
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J. INFECT DIS 0.0-0(1998)
EMBL; AFCD8027; 32659921; -.
NON_TER 51
NON_TER 551
SEQUENCY 551 AA: 61478 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       055346 PRELIMINARY: PRT: 1138 AA. 255346; PRELIMINARY: PRT: 1138 AA. 255346; PREMBERET 06, CPEATED) 01-JUN-1998 (TREMBERET 06, LAST SEGMENTE OPDATE) 01-TUN-1998 (TREMBERET 05, LAST ANNOTATION UPDATE) GLYCOPROTEIN G1 AND G2 PEECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEVIS & MORTHOU ST DEWE SABATINE M. STUDES TO STAND J. INFECT. DIS 0.0-0(1998).

EMBL: AF028024: 02653915: -.
SECUENCE 1138 AA. 127748 MW
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05-JUN-1998 (TREMBLREL. 05, CREATED)
01-JUN-1998 (TREMBIREL 05, LAST SEQUENCE UP
01-JUN-1998 (TREMBIREL 06 LAST ANNOTATION OF ANYTHER O
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       055343
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05, LAST SEQUENCE UPDATE)
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01-JUN 1998 (TREMBLEEL,
01-JUN-1998 (THEMBLEEL,
GLYCOPHULEIN G1 AND G2 P
PERGAMINO VIRUS,
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NON_TER
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206790;
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01-NOV-1996 (TREMBLEEL 01, LASI SEQUENCE UPDATE)
11-N-V-1996 (TREMBLEEL 01, LASI SEQUENCE UPDATE)
11-N-V-1996 (TREMBLEEL 01, LASI SEQUENCE UPDATE)
08E2 DELTAT. PYEFGLINE 5-CARBOXYLAYE REDUCTASE (FRAGMENT).
SACCHAPOMYCES CEPEVISIAE (BAKEP'S YEAST)
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES:
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NEUVILLE P., AIGLE M.:
"ore?, a mutation affecting proline biosynthesis in the "saccharomyces corovisiae, loads to a eds phonotype.";
MOL. GEN. GENET. 1744(1947-199(1994)).
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SABATTINI M., ST JEOR S.C.;
J INFECT DIS (0.0-0(1448)).
EMBL: AF028028; G2653923; -.
PARACENTROTUS LIVIDUS (COMMON SEA URCHIN).
TURARYOTA, METACOA, ECHINCOERMATA, ECHINGO
ECHINATEA, ECHINOTIA; ECHINIDAE; PARACENIA
                                                                                                                        01-NOV-1998 (TREMETER)
01-NOV-1998 (TREMETER)
01-NOV-1998 (TREMETER)
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                                                                                               CELL SURFACE PROTEIN
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NCE 258 AA; 29868
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OK, LAST SEQUENCE UPDATE)

OS, LAST ANNITATION UPDATE)

PRECUPSOR (FRAGMENT).
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01. LASI SEQUENCE CEDALE;
01. LASI ANNOTATION UPDALE;
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2: Mismatches
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77;
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COME 12424515; C. COME AND LEGATA ME
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"NUMBELL M., GLESKY T., SOCHER I., CORLESON A., GERANTON M.

"ADDRESON R. FAVELLO A., FULTON L. GARDNER A., GREEN P.,

HILLER E., JIER M., JOHNSTON L., JONES M., KERSHAW J.,

LAUSIER N., LATREILLE P., LIGHTNING J., LLOYD C.,

M. PEILMERE B., JEALLAGHAN M., PARSONS J., DERCY C.,

M. PORTON RE. B., JEALLAGHAN M., PARSONS J., DERCY C.,

M. PORTON R., SAUNDERS D., SHOWNREEN R., SWALDON N., SMITH A.,

SAUNDERA N., SAUNDERS D., SHOWNREEN R., WALDON N., SMITH A.,

E., STADEN K., SULSTON J., THIERRY-MIEG J., THOMAS K.,

VAUDERAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
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                                                                                                                                                                                                                                                                                                    84.8%; Score 28; DB
71.4%; Pred. No. 74;
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2: Mismatches
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BÜRFÜN J. CÜNNELL M. COPSEY T. COOPER J. CHUSON A. CRAXION M.
DERR S. DI Z. DOURRIN R. FAVETICO A. FULTON C. CAPEMER A. GREEN F.
HAWKINS T., HILLIER L. JIER M. JOHNSTON L. JONES X. KERSHAW J.
KIRSTEN J. LAISTER M. LAIFBEILLE P. LIGHTHING J. LOYD C.
KIRSTEN J. A. MORTIMORE B. O'CALLAGHAN M. PARSONS J. PERCY C.
PIEXEN L. POOPPA A. SAUNDERS D. SHOWNKEEN S. SMALUTN N. SMITH A.
SCHNHAMMER E. STADEN R. SUISTON J. HIERPY-MIEG J. THAMAS K.,
VAUGIN M. VAUGHAN K. WATERSTON D. MATSON A. WEINSTOCK L.,
WILKINSON-SPROAT J. WOHLDMAN P.;

"2.2 Mb of contiguous duclewallde Sequence from hermosome III of C.
SIGNAL.
                                 EMBL: L13654; G678547; -. PFAM: PF00141: peroxidase: 1
                                                                              01-NOV-1995 (TREMBLEREL 01, CREATED)
01-NOV-1996 (TREMBLEREL 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLEREL 05, LAST ANNOTATION UPLATE)
PEPOXICASE 1 PERCURSOR (EC 1.11.1.7).
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01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE;
01 NOV-1998 (TREMBLREL, 06, LAST ANNOTATION STRATE)
                                                                                                                                                                                                                                                                        INT PERSION ESCULENTUM (TOMATO)

EURAPYOTA: VIFIGIFIANIAE: CHAPGPHYTA/EMBEYGEPYIA GEGGT: EMBERTERYTA:
TRACHEOPHYTA; EURYLLOCHYTES: SEPRMATOPHYTA; MA NOLTOTHYTA:
EUTTCOTYLFDONS: ASTERITAE: SOLANANAE: SOLANALES: SOLANACEAE: SOLANANAE
                                                                                                                                                                                                                                                                                                                                                                                                            Q07446;
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EMBL: Z66563; E1322451;
SEQUENCE 2810 AA; <2
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EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                   MEDLINE;
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                        COMMENDIASE: SIPCOPRATEIN: PERSKIDASE; HEME: MODIFICHE
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HYPOTHETICAL 46.0 KD PROTEIN.
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SYNECHOCYSIIS SP. (STRAIN PCC 6803).
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EUKARYTTA VIRITIELANIAF, THAM-PHYTA/EMKRYCPHYTA GROUP;
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01-NOV-1998 (IREMBLREL, 08, IASI SEQUENCE UPDATE)
01-NOV-1998 (TERMBLREL, 08, IASI ANNOTATION HPDATE)
HYPOTHELICAL 35.1 KD PROTEIN.
  SEQUENCE FROM N.A TABATA S.;
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EUDICOTYLEIMINS; ROSIDAE; CAPPARALES; REASSICACEAE; ARABIDOPSIS
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Similarity 71.4%;
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Pred. No. 1e+02;
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KANDEO T SATO S
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HYPOTHETICAL PROTEIN.

ENGLEDION ORGANICAL PROCESS.
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TABATA S.;
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KIMURA T.,
OKUMURA S
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Copyright (c) 1893 - 1998 Compugen Ltd.

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Interferor gamma production inducer protein.
Interferor gamma inducer; IFNgamma; immunocomperent cells antiviral;
Interferor gamma; inducer; IFNgamma; immunocomperent cells antivirous;
antitumous; antiseptic; immunocegulatory; platelet-increasing agent:
thorapy, prevention, oscilyloma acumination, icial rancer; brain cancer;
granuloma; mycosis fungoldes; rheumatism; allergy; cytofoxicity; AINS;
hiller Toull, intuitoukino; IDS; tumour socrosis factor; IMF;
adoptive immunotherapy, monoclonal antibody.
                                                                      R99564;
29-SEP 1995 (first entry)
Human interferon-gamma inducer protein.
Interferon-gamma inducer protein: IEN-gamma; antiviral; "irucide: antitum-ur, antibasterial, immunorpadiator, adoptive inmunotherap
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Kohino K, Kunikata T. Kurimoto M. Okamura H,
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WFT, 96-079377/08.
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A to vol count protein (R99564) that induces interferon-gamma (IFN mamma) product by immunocompetent cells is the product of a CLEN mamma) product (IF24|1) derived from a human liver library.

Fix complete that of the china (see also T2409-10) and expression to linke that of the china (see also T2409-10) and expression to linke (If24|1) that was used to construct hybridoma H-1, which it breed out (IFN tumma inducer protein manualteral artitledy H IFAE (see If IF26-4-rection and purification of the inducer protein
                                                                                                                                                                                                                                                                                                                                                              Dicksp-19 on
Hamar mat in
Distorter
                                                                                                                          N PSER: T \in 4/2.
TWA - Tod. I dates between quality producting polypeptide - the at and present, e.g. viral disease, malignancies and i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAYB) BAYASHIBAPA SEIBUISU KAGAKU.
                                                                                                       Slot in S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HATACHIRGRA SELBUTSU KAGAKU.
S. Kedneck, Kerikata T. Eurimoto M.
hi M. Langweto T. Totidoe K. Ushio S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the interest out wiral disease, malignancies and immune
.ve 1 48pp; English
.ve 1 48pp; English
.ve 1 10 (Re9550) induces interferon-damma (IEN-damma)
.ve 1 and experent certs. It enhances the cytotoxicity of
.ve 1 induces the formation of killer cells (e.g.)

    (tilst entry)
    (tilst entry)
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Fred. No. 15:
: Mismatches
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Best Local Similarity
Troches 5: Conserve
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                                                     R99560
                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1995; 308055.
15-NOV-1994; JP-30A203.
23-FEB-1995; JP-058246.
10-MAR-1995; JP-078357.
18-SEP-1995; JP-26262.
29-SEP-1995; JP-274988.
R99560;
29-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic lacels). Recombinate IFM names inducet protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a merter carrying the enceding cDNA (732402). It is useful as an antiviral, antitumer, antibacterial, immunorcaulatory and blood platelet enhancing agent, and can be used in adoptive immunotherapy. It is also used to raise monocland; antitodies. A full-length sequence is given in R99560.
                                                                                                                                                                                                                                                                                                                A novel mouse protein (R9959) induces interferon-gamma (JEN-gamma) prodn. by immunocompetent cells. Its sequence was deduced from that of a cDNA clone (T72403) isolated from a mouse liver library. Recombinant IFN-gamma inducer protein can be profuced in high yields using host oralls, esp. Fechorichia coli, transformed with a rector can be profited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU. EVAkuda S. Kohno K. Kunikata T. Kur Taniquchi M. Tanimoto T. Torigoo K. Wpl: 95-25937/26.
                                 P99560 standard: Protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA convoling interferon damma productioduction polypoptide to treat and prevent, e.g. vital disease, maliquancies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-712931-A2
22-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon-gamma inducer protein; IFN-gamma; antiviral; virucides antitumour, antibacterial, immunorequiator, adeptive immunotibras
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                      carrying the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                            Example A-3-2; Page 36-37; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse mature interferon gamma inducer protein
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                                                                                                                            50 MYKDS 54
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100 09; Pred. No. 16;
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Pred. No. 16;
D; Mismatches
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                                                                                                                                                                                                                                DB 1; Length 157;
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Query Match
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30-NOV-1995
02-JUN-1994;
18-FFR-1994;
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18 SEP 1995;
29 SEP 1995;
                                                                                                                                         Wodel fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The mutility position of a farward human protein (899560) induces interferor gamma (IEN gamma) prode by immunocompatent cells is the prodoct of a cNNA clone (722424) obt3 from a human liver library. The protein ordinance the sylutoxicity of killer cells and/or induces the formation of killer cells (e.g. MK cells, lyaphoxim-mantizeting viller (AN) cells, and cytotoxic T-cells) the mantice protein (see also page 18, and cytotoxic T-cells) and titumor, antikenterial, immunoragulatory and blood glateler cohancior agent and can be used in adoptive immunotherapy. It is used to raise monoclonal antibudies.
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(HAYB) HAYASHHANAN SETRHTST KAMAKTI FOR KORDO K. KORDO K. KORDO K. K. Taniqueni K. T
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22-MAY-
Model for screening upds, for inhibition of recombinative in Liansforded with grame for ATPase under cortrol of inducible promoter Disclosure, Fla 2, Tap. German.
Helioubacter specific Almase genes 439, The
                                                                                                                                                                                                      WPI: 96-296831/29.
                                                                                                                                                                                                                                                                           (BYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09617066-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helioobaoter-specific ATPase; model; screening: metabolism
Helioobaoter pylori; ATPase; model; screening: metabolism
Decompositer pylori
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30-JAN-1997 (first
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Claim 5; Page 41-42;
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                                                                                                                                                                                                                                          ) BYK GULDEN LOMBERG
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c. foughty: 100.0%;
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58 442370
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TP-304203.
TP-058240
JP-078357.
JP-762662.
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109
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37. .193
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                                                                                                     inhibition of with gene for !
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       ٠<u>٠</u>
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RESULT W06103

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Host Tocal
                                                                               Matches
                                                                                                                Query Match
Best Local
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WFI; yb
                                                                                                                                                                                                                                                                                                                                            claim 33) Page 108-110; 156pp; English.
MR3 Nimera (MSC)2) is a fusion protein composed of bulbat hyelin basic protein (MSC)2) is a fusion protein (See also W00296) and felta PIPA (W00400), a proteclipid protein (PEP) matein that lacks hydrophobic domains 1 and 4 of native human PLP (W06106) but includes PLP aptropes associated with multiple sciences (MS). It can be expressed in a coli transformants using a bNA construct (T41802) conty the MSC21 select (F13902) conty the MS
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sclerosis
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MP3 chimwr: (MEP21 % delta PIP3 fusion).
MP3 chimwr: (MEP21 % delta PIP3 fusion).
Protectip1d protoin, PIP, delta PIP3 myelin basic protoin, MEP;
PROTECTIP1d protoin, PIP, delta PIP3 myelin basic protoin, MEP31.5 multiple solerosis, autoimmune disease; diagnosis;
MPP31.5 multiple solerosis, autoimmune disease; diagnosis;
MPP3 chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In T189°C, T19351 and T12142. These pages can be expressed usual heterological lests. When inserted into E. collinger a significant change in estabolism.

Sequence 686 AA:
                                                                                                                                                                                                                                                                                                               are useful of MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1995; US-431648
02-MAY-1995; US-431644
07-JUN-1995; US-482114
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ALEXION FHARM INC.
US DEPI HEALIH & HUMAN SERVICES.
US DEPI HEALIH & HUMAN HER Mueller EE.
MATIS L, MCFarland HF, Mueller EE.
WIlkins JA;
                                         Similarity 100.09;
5: Conservative of
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201. .385
/14bcl Doltu_F
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1. .197
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198. .200
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Pred. No.
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brod No 78;
Mishatches
                                                                          red. No. 42:
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"La [MBF21] delta FLP4 Lusion).
[13] Entroin PIP1 delta PLP3, myelin basic protein; MBP;
[14] Fibre scherosis, autoimmune disease, diagnosis,
[14] Fughhogte, Toell, uncray, apaptosis, MF3 chimera.
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/mater "PLP epitope associated with
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                                                                                            "sotes "PLP epitope associated with MS"
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"PLP epitope associated with MS"
"encephalitogenie epitope in mouse model"
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07-NOV-1996.
22-APR-1996: U05611.
02-MAY-1995: US-431648.
02-MAY-1995: US-431644.
07-JUN-1995: US-82114.
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/label= Epitope
/mote= "PLP apitopa
42. .62
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Chery Match 100.0%; Score 27, DB Best Local Similarity 100.0%; Prod. No. 41; Matches \S_\ell Conservative 0; Mismatches
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MM4 chimera (WÜNÜ3) is a fusion protein composed of human myolin basic protein (MBP) foetai isoform MBP21.5 (see also WÜÜ399) and delta PIP4 (WÖGAO) is proteinified protein (PIP) mutrim (that harks all 4 hydrophobic domains of native human PLP (WÜĞ100) but includes PLP epilopes associated with muttiple scients.5 (M5) in can be expressed in F collitransformants using a fine construct (T1893) could, the MBP21.5 delta FLP4 were factor. MP4 chicera and other scool PIP/MPP21 5 polyportides (WOOMS-140) WOOMS-180 are useful for the clinical assessment, diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (first entry)

DM4 Chimera (delta PLP4-MBP21.5 fusion).

Proteolipid protein; PLP4 delta PLP4; myelin basic protein; MEG:
MBP21.5; multiple sclerosis; autoimmune disease; disussess:
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Lenardo MJ, Matis L, McFarland HF, Mueller
Nye SH, Pelfrey CM, Squinto SP, Wilkins JA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-lymphocyte: T-cell; PM4 chimera.
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/note= "hexa-histidine tag facilitates recombinat"
protein purification"
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/hote= "encephalitogenic epitope in
369, 373
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/label= Epitope
/hote= "encephalitogenic epitope in house model"
292. .304
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/note= "PLP =pitope
                                                                                                                                                                                         /söte* "systhetic N*terminal the mative protein"
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                                                                                                                                                                                                                                                                                             /label- Delta-PLP4
                                                                                                                                                                                                                                                                                                                                                          /note= "preferred PM4 chimera
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22-NNP-1996. CC5611.
22-NNP-1995. CC56211.
02-MAY-1995. CC5-431644.
07-JUN-1995. CC5-43164.
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The Claim 35: Page 113-114: 156pp; English.

(W06101) and MBF21.5 (W00399). Delta PIP4 is a proteolipid protein (W06101) and MBF21.5 (W00399). Delta PIP4 is a proteolipid protein (PIP) mulein that lacks all 4 hydrophobic domains of native human PIP4 (W06106) but includes PIP epitopes associated with multiple sclorosis (W8). MRP01 is a frottal infirm of human rigid basic protein (W8). MRP01 is a frottal infirm of human rigid basic protein (W8). MRP01 is a frottal infirm of human rigid basic using a NAA construct (74894). The expressed in bacterial host cells using a NAA construct (74894). PIP polypeptides (see also would), W0F1 in the cambe expressed in bacterial host cells using a NAA construct (74894). PIP polypeptides (see also would), w0F1 in the clinical assessment.
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Hest Local Similarity 100.08;
Matches 5; Conservative 0
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Plotoclipid protein, PLF, delta PLP4, myelin basic protein;

MBP21 5: moltiple solerosis; autoimmune disease, diagnosis:

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w06lo5;
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From 15-117: 156pp: English.
From (Mag) behal isolorm MBPZL5 (see also M00399), the lost death isolorm MBPZL5 (see also M00399), the lost death is make impolin obligodondrocyte glycoprotein death isolored (Mn0101) a proroblipid protein (PLP) mulein.
From the lost death isolored by autoreactive Toells from the lost death isolored. MSS partners. The chimera was produced using notice (MSS) partners. The chimera was produced using notice (MSS) partners. The also T4.893). MN00694 chimera was produced in the lost of t
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                                                                                       lds.e%. Score 27.
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                                                          core 27. DB 1. Length 492. red. No. 55; Mismatches 0: Indels
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EEE SKKKK DE DAG
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07-NOV-1946.

22 AFR 1996; U05611.

02-MAY-1995; US-431648.

02-MAY-1995; US-431644.

07-JUN-1995; US-482114.
                                Foetal myclin basic protein MBF+X20ys81/bact. Wyelin basic protein MRF-X20ys81, protectived protein: multiple sclerosis; autoimmune disease; diagnosis; therapy: Tiymphboyte; Ticoll; anerqy; apoptosis. Synthetic.
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The notive human 21.5 FE4 towtal isoform (W0034-) of notion (X2) that protein MBP+X2Cys81; includes at extra 2-encode; retion (X2) that may contain an epitope involved in the pathwagenesis of multiple solerosis (M3), the X2 region is not found in the MBP of healthy solerosis (M3), the X2 region is not found in the MBP of healthy solerosis (M3), the X2 region is not found in the MBP of healthy solerosis (M3), the X2 region is not found in the MBP of healthy solerosis (M5), the X2 region is not found in the MBP of healthy solerosis (M5), the X2 region is not found in the MBP of healthy solerosis (M5), the X2 region is not found in the MBP of healthy solerosis (M5), the X2 region is not found in the MBP of healthy solerosis (M5), the X2 region is not found in the MBP of healthy solerosis (M5).
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Horin Tyelle basic Fritch Mpp MRP-X20y-81 Fritchleid protoin: Fifth multiple sclerosis; autoimmune disease; diagnosis: therapy: T-lymphocyte; T-cell: anergy: apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thirlls for responsiveness to MBP epitopes and can be used as therappointic agents that but by inducing T cell responses, including anergy and apoptosis, as a means of treating MS. Sequence 197 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lenardo MJ, Matis
Nye SH: Pelfrey CM.
region
                                                                                                                                Ol-FER-1997 (first entry)
                                                                                                                                                  W06107;
                                                                                                                                                                  W06107 Standard, Protein, 203 AA.
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(USSH ) US DEPT HEALTH & F
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01-FEB-1997
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                                                                                                                                                                                                                                                                       58 SCHANN RE
                                                                                                                                                                                                                                                                                         1 MYKDS 5
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81
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  Location/Qualifiers
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60. .85
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Pred. No. 21;
0: Mismatches
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N W09634522-A1.

PD 07-NGV-1996.

PF 22-APR-1996: U05611.

PF 02-MAY-1995: US-431644.

PR 07-JUN-1995: US-431644.

PA (ALEX-) ALEXION PHAPM INC
PA (GSSH ) US DEFI HEALTH & HUMAN SEPVICES.

LEGATION MJ. NATIS I. MCCATIAND HF, Mueller EE.

LEGATON MJ. NATIS I. MCCATIAND HF, Mueller EE.

- SH. Felfiery CH. Squinto SF, Wilkins JA:

- SH. Felfiery CH. Squintein and proteolipical dispersion and p
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07-NOW ]906
07-NOW ]906
20-APP1996: U00611
02-MAY-1996: US-431644
07-JUN 1996: US-431644
07-JUN 1996:
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A 21.5 kDa foetal isoform (W06107) of myelin basic protein, M6P+X2/1981/Page; is the product of a ENA construct (T41846) based on the human foetal MBP+X2/1981 isoform (W0399) but utilising bacterially-preferred codons in place of the native human codons (see also T41889). This increases produce of the MBP in E. coll by at least five Ecombinant MBF 11.5 polypeptides (see also W00/99 and W05109) are useful in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Koy
region
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Wyells basis protoin, XPP: MES-X2Sox91; protoilipid protoin; multiple sclerosis, autoimmune disease, diagnosis; therapy; Triymphorits, Toroil, prorgy, profitsis.
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                                                                                                                         New human myello lasic protein and proteolipid protein variant(s) used in the assersment diagnosis and treatment of multiple
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/Taiole N2
/Motes "Exon 2 encoded region, with Gys81Ser
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/to-te= "the hexa-histidine tag familitates
purification of the recombinant protein
from host cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation"
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Pred. No. 21;
0, Mismatches
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RESULT
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Best Local
Matches
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Best Local Similarity
Matches 5, Conserv
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17-JUN 1997
24-JAN 1996; 028722.
04-0CT 1995; JP-279906.
10-MAP-1995; JP-078367.
29-SEP-1995; JP-274998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liscissury Fage 82-83, 155pg, English.
A 215 kDa feetal Issform (W05108) of myelin basic pritoto, M8F-XISER3, bact., is the product of a DNA constitut (11.837) based on the human feetal M8P+XZOY881 issform (W00399) but utilising codons that are highly expressed in bactorial genus in place of the native codons (see also 741889) and incorporating a sequence coding for a hexa-histidine tail. This allows large-scale produced multification of the M8P in bacterial bosts. Focombinant MRF 215 polypegiides (see also W1614 and w26137) are useful in the colored assersement, diagnosis and treatment of M8.
    15-007-1997 (first entry)
Human protein for induction of interferon-gamma.
Interferon-gamma: immunocompetent cell; malignant tumour;
wiral disease; banterial infention, immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T80210.
A drug containing a polypertude which induces
useful for treating e.g. malignant tumours, vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine protein for induction of interferon-gamma.
Interferon-gamma, immunocompetent cell, malignant tumour;
vital dispase; bactuital infection; immune disease.
                                                         W24258 standard; Protein; 157 AA W24258; 15-007-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                  This sequence impresents a protein which induces interferon-damma production in immunicarpoint talls. This protein and two codes the major component in a drug for the prevention and two-chart of a malignant turmours, "Iral diseases, banterial infections and
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15-0CT-1997
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97-keykyl/34.
sapiens
                                                                                                                                                                                                                                                                                                      diseases.
ce 157 AA;
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Pred No 16;
Mismatches
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viral, bacterial o
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Perfect score:
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():Superfamily: myelic basic protein
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A.Title Pepcitive DNA (TGJA): 5' L5 the human my lin back problem analysis of a Reference number: 154219; MUID:90152679
A.Racession: 154219
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E.Both, H.J. Kischalist, N.E. Kelleto do Bosbo, N.: Crans
J. Neurosci. Res. 17, 221-328, 1987
A.Title. Evidence for the expression of four myolic tari-
Alecteroco number (156567; MUID.87311781
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                                                                                                                                                                                                                                                       R;Boulias, C.; Pang, H.; Mastronardi, F.; Moscarello, M.A.
Arch. Biochem. Biophys. 322, 174–182, 1995
A:Title: The isolation and characterization of four myelin hasic proteins from
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F.F.II, H J , Fronquist, K., Preterius, P.J., Crandall, E.L.,
J. Neurosci. Res. 16, 227-238, 1986
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J. Biol. Chem. 264, 5121-5127, 1989
A.Title. The Reclation, characterization
A:Reference number: A33273: MUID:89174797
A:Accession: A33273
                                                                                                                  A;Cross-references: GDB:119379; GMIM:159430
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A; Residues: 1-59,86-133,145-197 <RE4>
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A. Feference number: 156565, MUID:86308101
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A;Molecule type: DNA
A;Residues: 1-59 <RES>
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A.Molecule types mENA
A.Rosibuss 194.074 916-309-306W19
A.Gross-reference GR-M15060-NID
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A.Expotitional Scurpes Cillo M722.
A.Accession: B26591
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Althouse references. GB.MIIJ38, NID.4199044, EID-4387414
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A)Accession: A45421
A)Molecule type: mENA
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A.Grose troft is over 1988 337
A.Revidsor | 1986 17AM197 | VII 17AM194
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A.Posibuos: 1-191. (SREP)
A.Posibuos: 1-191. (SREP)
A.Posibuos: 1-191. (SREP)
A.Potoss-references: EMEL:X67319; NID:g51332: PID:g51333
A.Potos submitted to the EMEL Data Library, July 1992
A.Poto: Submitted to the EMEL Data Library, July 1992
B.Zollor, M.K.: Hunkeler, M.J.: Campagnoni, A.T.: Spraguo, J.: Lazzarini, B.A.
Proo. Natl. Acad. Sol. U.S.A. 81 18-22, 1984
A.Title Characterization of must myolin
A.Foforoice 6.mber: 10e/90; MUII.34119431
A.Accession: 158996
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A.Fxperimental source M41. splice form 14K
A.Fxperimental source M41. splice form 14K
T. Neurochem. 59, 2318 2327, 1992
A.Fitle: A novel transcript overlapping the myelin basic protein A.Reference number: 148407, MUID:93057597
A.A.Accession: 148407
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A.T. The profitch elements of the mease myellh basic protoin A.Feference number. 156-22, MIKLEY-52919
A.Accession. 154033
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A:Mostatis [219-248] VZEL
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C:Accession: G64618

B:Tomb. J.F.: White, 0:; Kerlavage A.P.: Clayton, 9.A.: Sutton, G.C.: Sloiselmann, 8. Peterson, S., Defras B. Richardson, 5: Fullson, 8: Modo son, J.D.: Kelky, J.M.: Cotton, M.D.: Weidhan, J.M.: rujii. 0: Romann. Marthey. Nature 388, 539-547, 1997

Nature 388, 539-547, 1997

A:Authors: Hayes W.S.: Recordovsky, M.; Karpk, P.D.: Smith, H.O.: Pymer. C.M. Vento A: Title: The complete accounts sequence of the dasting pathward Hediculosofter public A: Records for Mode accession 664618

A:Accession 664618
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C/Superfamily: heat shock protein 70
C/Keywords, ATP, molecular chaperone
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B:Wallich, R.; Helmes, C.; Kramer, M.D.; Simon, M.M.
submitted to the EMBL Data Library, August 1992
A:Pegeription: Characterization of an HSP78 related protein that is the A:Reference number: S25155
A.Accession, S25155
A:Mulecule type: DNA
A:Residues: 1-743 <ANN
A:Residues: 1-743 <ANN
A:Experimental source: strain 52880
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C.Species Helicobarten pyloni
C.Sate 09 Aug 1997 ##eaper=n_revision 09 Aug 1997 #% at_cluste 17 711 199
C.Sate 09 Aug 1997 ##eaper=n_revision 09 Aug 1997 #% at_cluste 17 711 199
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A;Accession: $38143
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A: Bosidues: 1-635 <WALS
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A: Residues: 1-635 <TIL>
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Date: (3.Mag.1994 #soqueron_remision = 0.Mag.1994 #to.kt_change
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Local Similarity 100.0%; Pred. No. 53;
hes 5; Conservativo 0; Mismatchon
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    Mismatches

                                                        NID.9486536, 115.44665 -
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Cracession, 207363
R.Bagheb, J.A.: Dottin, R.P.
R.Bagheb, J.A.: Dottin, R.P.
R.Deir Ards Reg. 15 Register of a UDF glucuse pyrophosphorylase gene of Dictyostclium
A.Hitie: Structure and sequence of a UDF glucuse pyrophosphorylase gene of Dictyostclium
A.Reference number: S07363; MOID:87231075
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A:Molecule type: mRNA
A:Pesidues: 1-142 -68A
A:Cress:references PME
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ArMap position: 11s
OrKeywords: transment:and
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A:Residues: 1-511 <RAG>
A:Cross:references: EMBL:Y00145: NID:g7384: P1D:g7385
C:Commont. This enzyme datalyses alpha-D glucose-1-ph
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Best [ona] Similarity
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:Date: [0-Apt-]996 #sequence_revision 19-Apt-1996 #text_change 10-Sep-1997
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Best Local Similarity 100 0%:
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Mol.
A:Gross-references OF 100057, NED-g349021, PED-g3490702
0.Saporfanily, horpostrus liboudochooside diphosphate leducture large
O:Kepwords Jeokyribachie-13-kin-sperhesis, baidire Juitage, redix-a
F:217-440,700-800yDiscifide books redox-active status fredicted
F:425,429/A-mive site Aso. Six status predicted
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A;Molecule type: DNA
A;Festilues 1:804 (BTE)
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C:Superfamily, herpesvirus ribonucleoside-diphosphate reductase
C:Keywords: DNA replication; oxidoreductase
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A.Title: The cell byole genew ideal, and smoller, of the fission peast Schimo. A:Peforence number: $34807
A.Accession, 334807
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A.Pesidues: 1-792 PCAS:
C.Suprifamily, herpesitive illumidenside diphosphate inductive
C.Koywerds: CNA replication, uxidoreductase
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A:Mejoronge mumbers Ac4050; MCID:Engo7721
A:Accession: A24050
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REMUTEDBY, L., Niblett, D.: Harris, D. submitted to the EMBL Data Library, November 1995 A:Reference number: 862573
A.Accession, 862577
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NAIternate mames: protein SARCIP7.05
C.Species, Schizosacchardmyces pombe
C.Species 10 May 1916 # September Dembe
C.Accession: $62577
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A.Map position: 11p15.5-11p15.4
C:Superfamily: herpesvirus ribonucleoside-diphosphare reductase large curic.
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Search completed: June 22, 1999, 10:58:48 Job time: 147 sec
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C.Superfamily, herpesylfus fiberurlenside-diphosphate reductase large chain
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A:Residues: 1-811 <MUR>
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Best Local Similarity
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Matches 4: Conservative
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1 1431_ENTH: STANDARD, PRT, 239

1 01-NOV-1995 (REL. 32, CREATED)

1 01-NOV-1995 (REL. 32, LAST SPECIENCE UPDA

1 01-NOV-1997 (REL. 35, LAST ANNOTATION UP

1 01-NOV-1997 (REL. 35, LAST ANNOTATION UP

2 ENTANCEBA HISTOLYTICA, SAFOLMASIISUPHUPA:
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01-DEC-1392
01-DEC-1392
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SAMUELS:N T. SHEN P. MECKLER 3. DESCOTEAUX S. EC.
SAMUELS:N T. SHEN P. MECKLER 3. DESCOTEAUX S. EC.
SUPMITTEL (A'5':14-4) T. EMFL/GENEAUK, CLEL CAIA FAMES.
T- SIMILARITY: BELONGS TO THE 14-3-3 FAMILY.
EMBL; U13418; G571361; T.
EMBL; U13418; U13418; T.
EMBL; U1
WALLICH R., HELMES C., SCHAIBLE U.E., KRAMER M.D., SIMON M.M.; INFECT. IMMUN. 60:4856-4856(1992).
-!- FUNCTION: ACIS AS A CHAPPRONE (BY -!- INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                      STRAIN=2S7
MEDLINE: 9
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STRAIN=15ULATE CA12;
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PROKARYOTA: GRACITUTUTES: SCOTOBACTERIA: SPIROCHETES:
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TRANSMEM
TRANSMEM
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                                                                             CYTOKINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                         CELLS
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Query Match
Best Local Similarity 100.0%;
Matches 5: Conservative 0
                                           EMBL: D49950:
EMBL: U90434;
MIM: 600953;
                                                                                                  TISSUE-PERIPHERAL BLOOD: CONTICK, JOH T.H.;
CONTICK, KIM S.J., TINTICL, CHUN H.S., JOH T.H.;
SUBMITTED (FEB-1997) IN EMBLATENHANK/1995 LAIA MANKS.
-(+ FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPER-
AND STIMULATES INTERFERON GAMMA FROMSTION IN THELPER
                                                                                                                                                                                                                                                                                                                                                                      014116;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
1CHTERLEUKIN-18 PRFCHPSOP (TI-18) (INTEREPREON-GAMMA INDUCING FACTOR)
(IFN-GAMMA INDUCING FACTOR) (INTEPLEUKIN-1 GAMMA) (IL-1 SAMMA).
IL18 OR IGIF.
                                                                                                                                                                                                       MEDLINE: 96247646.
USHIO S., NAMBA M., OKURA T., HATTORI K.,
TANABE E., KONISHI K. MICALLEF M., FUJII
EUKUDA S., IKEDA M., OKAMURA H., KURIMOTO
J., IMMUHOL. 156.4274-4279(1996).
                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN)
EUKARYOTA, METACOA, (
ETTHERIA, FRIMATES.
                                                                                                                                                                             [2]
SEQUENCE OF 2-193 FROM N.A.
                                                                                                                                                                                                                                                                                    TISSUE-LIVER
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                          D49950;
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    37
                                                             G1899242;
                                                                          G1405319;
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75012 MW;
   193
961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H4 (POTENITAL).

H5 (POTENITAL).

H6 (POTENITAL).

H6 (POTENITAL).

CYTOPLASMIC (POTENITAL).

PHOSPHORYLATION (PEDARIF).

E -> K (IN REF. 1).

K -> R (IN REF. 1).

I -> V (IN REF. 1).

Y -> A (IN REF. 1).

M -> A (IN REF. 1).

Y -> I (IN REF. 1).

V -> I (IN REF. 1).
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BY SIMILARITY.
INTERLEUKIN-18
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H1 (POTENTIAL).
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Pred. No. 34;
Mismatches (
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H2 (POTENTIAL).
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                                                                                                                                                                                                                        NUKADA
M., F.:
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                                                                                                                   IN SPLEEN CELLS
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           RESULT ILL18_PROBULT OF CONTROLS OF CONTRO
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Best Local
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MEDLINE, 97174446.
LPIG STANDARD: PRT: 150 AA
019073;
15-UU-1998 (REL 36 GREATED)
15-UU-1998 (REL 36 LAST SEQUENCE UPDATE)
15-UU-1998 (REL 36 LAST ANNOTATION UPDATE)
15-UUL-1998 (REL 36 LAST ANNOTATION UPDATE)
INTERLEUKON-JA PARTURAJA (II-S) (INTEREENON-JAMMA INTENTIOP)
INTERLEUKON-JA PARTURAJA (II-S) (INTEREENON-JAMMA INTENTIOP)
(ITAY-GAMMA-INDUCING FACTOR) (INTERLEUKIN-I GAMMA) (IL-1 GAMMA)
(FRAGMENT)
IL18 OR IGIF.

SUS SCRIFA (FIG.)
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CONFLICT
TECTENTE
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1118_WC.SE
P70380:
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TANIMOTO I., TORIGOE K., OKURA I., NUKADA Y., HATTORI K.,
AKITA K., NAMBA M., TANARF F., KUNISHI K., FUKUDA S., KURIMUTJ M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE:
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EURARYVIA: METAZUA: CHURDATA: VEKTERRATA: TETRAPUDA: MAMMALTA:
EUTHERTA: RODENTTA.
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(IEN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
IL18 OR IGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.83..338
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTEFESSERIAL PARTIES (IL-1P) (INTEFES N.-SAMMA INCOINS FAST 4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 MYKUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLIN. INVEST. 99-469-474(1997).
- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND SIMULATES INTERFERON SAMMA PROPUCTION IN I HELPER TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
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5 Tokart
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Similarity
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دو دمو
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Fred. No. 8.9;
O: Mismatches
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ACASTASA CROSS
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Pred. No. 9;
Mismatches
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د.
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       독목목중
                                                                                                                                                                              MBF_HUMAN
                                                                                                                                                                                                                      RESULT
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Best Loc
Matches
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Best Local Similarity 100
Marries & Trascreation
MBF_HTMAN
PU2686;
21+JHF=1486
01+NOV-1991
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
NON_TER
SE_CENCE
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VARSELIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOSS L.L. MUFRAUGH M.P.:
SUBMITTED (JUL-1997) TO EMEL/GENEANK/DUEJ DATA BANKS.
-!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN I HELPER TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTER , JAHNG J.W. TINTI C., SON J.H., JOH T.H.:
1 HEGE CHEM, LTLICAGE LOTS (1897).
1 FUNCTION APPRENTS MATERAL KELLER OFFIC ACTIVITY
AND STIMPLATES INTERFRENCY GAMMA PRODUCTION IN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY: MEDLINE: 97152963.
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EURAPYTA, METACIA, THISTATA,
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L; U68701; G2228534; -.
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MISSING (IN 180FORM ALPHA)
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Pred. No.
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Pred. No. 7.3;
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MCKNEALLY S.S., CHOU F., KIRLER
EM. .15.46(0) 4640(1971)
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                                                                                                                                                                                                                       12 (1-1-74 (1991)
1811 FE HILM MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
                                                                                                        CAR CARTON: CYTOPLASMIC SIDE OF MYELIN.

OF PRODUCTS: HUMANS HAVE THEFE FORMS OF MEP,

ARCHDOANT), AND 17.2K. THE THREE FORMS ARE P
                                                                                                                                                                                                                                                                                           AVERS TIME, POPKER BI, TAKAHASHI NI, HOOD LIE.,
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                                                                                        TOTAL STATE
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ACETYLATION (MONO-:5% OR DI-:50%)
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Best Local Similarity
5: Consort
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SEQUENCE
                                                                                                                                   -11 SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYHLIN.
-11 ALTERNATIVE PRODUCTS: MOUSE HAS FOUR FOUNDS OF MAP. 21.5KD.
-17KD, AND 14KD, PKESENI IN KELATIVE AMOUNTS OF 1:10:3.5:35.
-1 THE SEQUENCE SHOWN IS THAT OF THE 21.5KD FORM.
                                                                                                                                                                                                                                                                                                                                                                DE FERRAL LAZZARINI R.A.;
LAZZARINI R.A.;
TTT: 49.721-727(1985).
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                                                                                                                                                                                                                                                                                                                   TAKAHASHI N., ROACH A., CELL 42:139-148(1985).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (18.5 KD FORM). MEDLINE; 85254913.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ALL FOUR FORMS). MEDLINE; 86079555.
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20-MAR-1987 (REL.
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       M11533 G387414
M11529 G387714
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TAMURA T.A.,
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RODENTIA.
                                                                                                                                                                                                                                                                           KITAMUPA K
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196 /
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  G387415;
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JOINED
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                     JOINED
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0A8864EE CRC32;
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MISSING (IN 18.5 KD FORM AND 17.2
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                                                                       [2]
SEQUENCE OF 29
TISSUE=T-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                             FERNIMOUSE STANDARD. FRT. 29
P22005;
01-AUG-1991 (REL. 19, CREATED)
01-AUG-1997 (REL. 19 IAST SECURENCE UP
01-NUV-1997 (REL. 35. LAST ANNOTATION
PROCENCETALLY A FRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _MOUSE
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VARSPLIC
                                                                                                                                            MEDLINE: 90287163.
KIIPATPICK D. I. ZINN S.A., FITZGER, MEYERHARDI J.;
MOT CELL BIOL 10:3717-3726(1990)
MEDLINE: 86179902.
TTPAMERI G PEMER
LEE F.D.;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA
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MISSING (IN 17 KD FORM AND 14 KD
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Pred. No. 9;
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RESULT 11
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01-NOV-1986 (REL. 03, LAST SEQUENCE UP
01-NOV-1987 (REL. 35, LAST ANNOTATION
PROENKEPHALIN A PRECURSOR.
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SIGNAL
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TITSTE SPECIMITY FROMWALLIAMIN SCHAFTE GELLS.

TOTSTE SPECIMITY FROMWALLIAMIN SPECIMINATE GELLS.

TORVELORMENTAL STACE HIGHEST EXPRESSION IN LATE PACHYTENE SPECIMATOGYTES AND POSIMETOTIC FOUND SPECIME CYSTETINES THOUGHT THE THE N-TERMINAL CONTAINS 6 CONSERVED CYSTETINES THOUGHT THE FUNCLUES AND PECCESSING.

HE INVOLVED IN POSIMETICS FUNCLUS AND/HE PECCESSING.

SIMILABILY ECONS THE FOUND NITH FROM THE PECCESSING.
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MEDLINE, 85063850.
HOWELLS P 0 FILPATPYON F 1 PHAIL P MOMAHAN
UDENERIEND S.:
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PROSITE: PS/1252; OPICIOS
GLEAVAGE ON PAIR OF BASIC
   FOSEN H., DOTO
FOSEN H., DOTO
                      SEQUENCE FROM N.A. MEDLINE: 85054888.
                                                     YOSHIKAWA K., FEBS LETT 24
                                                                     SEQUENCE FROM N.A. STRAIN=WISTAR; TIS MEDLINE; 89211398.
                                                                                                                                     TISSUE-BRAIN
MEDLINE: 850
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BUKARYOTA: METAZOA: OHOPDATA: VERTEBRATA; TETRAPODA; MAMMALIA;
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EMBL; M55181; G201034; -.
EMBL; M12227; G387143; -.
PIR: B35678; B35678.
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DOUGLASS J., HERBERT E.;
HEM. 259:14309-14313(1984)
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                                                   K., MARUYAMA K., F
246:193-196(1989)
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                                                             AIZAWA T.,
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MET-ENKEPHALIN 2.

MET-ENKEPHALIN 3.5EEF-LEU.

MET-ENKEPHALIN 4.

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LEU-ENKEPHALIN AEG-PHE.
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MISSING (IN REF. 2).
THUSTER) TROP2;
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METCHNE, THE ZETTIN G.E., METER I., HAHLBROCK K., SOMSSICH I E.,

KOPEDAGE T. FREZINI G.E., METER I., HAHLBROCK K., SOMSSICH I E.,

KOPEDAGE TOR (1994).

TEAN CENT. N. SECTIFICACIAN BINDS TO THE FUNGAL ELICITOR-RESPONSIVE

INA EL MONT. TAATITUTA S., SETTHE SIENE EFO TRANSFER

LONGEROTIAR CONTINUE NUCLEAR.
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THE A TRANSPORT EXPRESSED IN BRAIN, HEART AND TESTIS.

THE A TERMINAL CONTAINS A CONSERVED CYSTEINES THOUGHT ON LOVE IN LIBERTHOUGHT BANGOR PROGRESSING.

ARTIVE RELAXION ROTHER OFFICER NOW PROTTERS PROCHESORS.
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YE SE PATROJEN INFECTION.

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YE TELP.
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latify 100.0%: Pred. No. 13:
Conservative 0: Mismatches
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(REST RECORDANCE SEGMENCE UPDATE)
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MET ENKEPHALIN 3.

MET ENKEPHALIN - ARG-GLY-LEU.

MET ENKEPHALIN - ARG-GLY-LEU.

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MET ENKEPHALIN - ARG-PHF

L -> V (IN REF. 3 AND 4).
ALT BUNK (BY SIMILARITY)
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VAN VLIET-REEDIJK J.C., PLANTA R.J.;
SURMITIEL (MAP-1994) TO EMBLYSENFANK (1984 PATA FANKS,
SURMITIEL (MAP-1994) TO EMBLYSENFANK (1984 PATA FANKS,
1 STROEL HAF LOCATION, INTEGRAL MEMBRANE PROTEIN (FROBANCE).
1 STROEL ALBY STRONG, TO YEAST YBLOTTW.
EMBL, 228932, G486537;
PIR: S38143: S38143.
PIR: S38143: S38143.
FRANSMEM 31 55 POTENTIAL.
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TRANSMEM 31 55 POTENTIAL.
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01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 83.6 KD PROTEIN IN CCP1-MET1 INTERCENS: FEGI
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3-2.
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(TYPE C).
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2 x 13 AA
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2 x 2 AA
2-1.
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(TYPE C).
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Best Local S
Matches 4
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MEDILNE: 98083068.
SADOWSKY M.J. TENO 2., DE SCUZA M., WACKETT L.F.,

J. BACTERIOL. 180:152-158(1998).
J. BACTERION. TRANSFORMS N-180PROPYLAMMELIDE TO GYANURIC ACID AND
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ATZC_PSESD STANDARD: PRT: 403 AA.
ATZC_PSESD STANDARD:
PSESD STANDARD: PRT: 403 AA.
ATZC_PSESD STANDARD:
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
N-ISOPHOPYLAMMETINE ISOPHOPYL AMINOTATION (EC 3.5.1.-).
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P22552;
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1- FATHWAY: HEIRD STEP IN AIRAZINE DEGRADATION PATHWAY.

1- SUBCELLIAR LOCATION: CYTOPLASMIC (POTENTIAL).

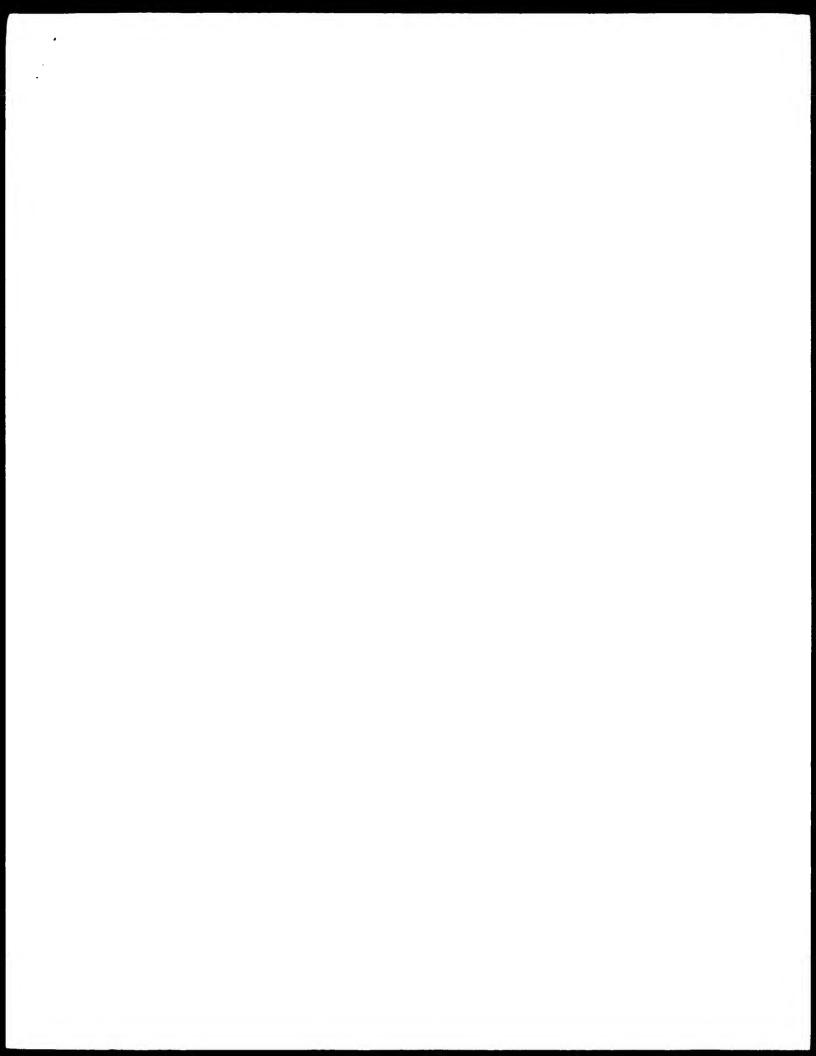
1- SIMILARITY BRIOMS TO THE N-ACYL-D-AMING-ACID DEACYLASE FAMILY REBLIA AF017572: C27786101: -.
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01-MUG-1991 (REL. 19, LASI SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LASI ANNOTATION UPDATE)
ATP_SYNTHASE ALPHA CHAIN (EC 3.6.1.34).
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PROKARYOTA: GRAFILICHIES: SOUTOHACTERIA: AEROBIC
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267 LYKDS 271
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80.0%;
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1: Mismatches
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Pred. No. 1.6e+02; 
1: Mismatches 0;
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Search completed: June

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1999, 10:59:45

Job time: 71 sec



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the soure of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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KIESIEN I CALGER M. CAREFILLE P. I.IGHINING T. LUCYD C.,
MCMCHRAY A. MCKIE H. C'CALLAGHAN M. PAKSONG J. PERCY C.,
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CHYPHANTET ACT N. STORY O. HIEFPY-MIES I. THOMAS F.
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S ÇENTLA: STURGEMATHI: MURIDAE: MURINAE; RATTUS.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TPEMBIPEL OF CREATED)
01-JUN-1998 (TREMBIPEL OF LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBIPEL OF LAST ANNOTATION HEDATE)
HYPOTHETICAL 120 7 KD PROTEIN CITH9-LOC IN CHRUMOSOME 1.
SPAC17H9-LOC.
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REVUSLTA J.E., TIMINEZ A., BALLESTA J.F.G., DEL REY F.,
SURMITTERO (FEB-1996) TO EMBL/GENHANK/DDBJ DATA BANKS.
EMBL. 77419 ECT9037; -
EMBL: X95644; E223185; -
SEQUENCE 150 AA; 16771 MW; 17086946 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

RACLESTA T PG REMATHA M SOLER-MIRA A., JIMENES A.

RACLESTA T PG REMATHA M SOLER-MIRA A., JIMENES A.

RACHTA-TANTALETT T M RESKEWICT T EFT KEY F., KEYCETTA

BUITRACO M J., SANS J P.;

ROTHRACO M J., SANS J P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHIZOSACCHAPOMYCES POMBE (FISSION YEAST).
EUKAPYOTA: FUNCI: ASCOMYCOTA: APCHIASCOMYCETES:
SCHIZOSACCHAPOMYCETALES: SCHIZOSACCHAPOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ** SIMILARITY: SOME, TO HUMAN UV-DAMAGED DNA BINDING FACTOR (UT$280) EMBL: 298597; E334303; *,  
HYPOTHETICAL PROTEIN: DNA REPAIR: SEQUENCE 1037 AA: 120654 MW; **7712685 CKT12*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKELTON I CHURCHER C M. BARRELL R G., BAJANDREAM M.A., WOOLSUBMILIEU (AUG-1997) TO EMBL/GENHANK/DUBJ DATA BANKS.
-1- FUNCTION: MAY HAVE A ROLE IN DNA REPAIR.
                         01-NOV-1996 (IREMBIREL
01-NOV-1996 (TREMBIREL
61-AUS-1948 (IREMBIREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                         FEELIMINAFY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.9%;
80.0%;
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01. CYEATED)
01. LAST SEQUENCE UPDATE)
H2. LAST ANNUTALION UPDAT
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Pred. No. 7.4e+H2;
1: Mismatches (
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Pred. No. 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Best Cons. &
Matches 4
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Best Local Similarity on o
Total Armonistry
SEQUENCE FROM N.A.

WILSON R AINSTRUME R ANDERSON K, BAYNES C, REPKS M, BONFIELD J.

WILSON R AINSTRUME R ANDERSON K, BAYNES C, REPKS M, BONFIELD J.

BURT N T TO NURE! M CODSEY T COOPER J. COULSON A, CRAXYON M.,

DEAR S | DUT Z DURRIN R , PAVELLO A | FULTON T , GAPDNER A , GREEN P

HARKINS T HILLER I, TIEF M , JOHNSTON L , NONES M., KERSHAW J.,

KIPSTEN T | LAISTEP N LATPETILLE P LIGHTNING J , LLOYD C ,

MCMGRRAT A., MORTIMORE R , O'CALLAGHAN M., PARSONS J., PERCY C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL. AF079530, G 511283, ...
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SUBMITTED (MAY-1998) TO EMBL/GENBANK/UUSU DAIA FANKS
EMBL OTERA GARITS
TITLE TO TANA GRADE MW. CSEYA950 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL 08, CREATED)
01-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDAT
SLIAL CELLS MISSING PROTEIN HOMOTOG
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CUMARYOTA METACOA, OHOSCATA, VERTEBRATA, MAMMALIA EUTHERTA
                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS
EUKASYTTA METATTA MET
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C1-JAN 1999 (TREMBLEEL
91-JAN-1998 (TREMBLEEL,
01-NOV-1998 (TREMBLEEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANENTEA Y STEATA S CHRISET I TOTATTO S MOSE E
MANASAKI M., FUSHIKI S., ARITA N
"MOLECITAL CLUBIO Of a human train homelegum of glial
(MGMM)."
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EUKABYCTA FUNCI, ASCO
                                                                                                                                                                                                                                                            RHABUITINA
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MEL AJELLOMYCES:
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လို့ ရှိ
                                                                                                                                                                                                                                                         TIA SECTEBRISTEA FHABRITIA, PHABRITISA; PHARRITITAS; PHARRITITOAE; PRICIDERINAE; CAENORHABDITIS
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1: Mismatche
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred No. 3 Re+02,
1: Mismatches 0;
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                                                                                                                                                                              Matches
                                                                                                                                                                                                      Guery Match
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STEMILIEF (LET 1977) T. EMEL.
STEMILIEF (LET 1977) T. EMEL.
EMBL: U42848; G1125818; T.
STECTION B. 187 AA. 22841 MM.
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01-NOV-1998 (TREMELREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMELREL 08, LAST ANNOTATION UPDATE)
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Q18337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans.":
NATURE 368:32-28(1994).
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                                                                            131 LYKDS 135
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                                                                                                                                                                              4, Conservative
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                                                                                                                                                                                                      TABL, TEMBANE, TIBY DATA PANKS
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1, Mismallhus
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1. Mismatches
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045176; 045176;

PRELIMINARY:

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Lordy March

Nest Lord Smilarity

Takens 4 Tenority
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N V-19 (TRAMSCHELL S), LAST SEQUENCE OPDATE)
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THE V-19 (TRAMSCHELL S), LAST ANNOTATION OPDATE)
THE V-19 (TRAMSCHELL S), LAST ANNOTATION OPDATE)
THE V-19 (TRAMSCHELL S), TRAMSCHALL HEARPSOAL INSECTA:
THE V-17 (TRAMSCHELL S), TRAMSCHALL HEARPSOAL INSECTA:
THE V-17 (TRAMSCHELL S), TRAMSCHALL SATURNITUAE: SATURNITUAE:
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WELL SALE
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                                                                                                                                                                                                                                                                                                                                             SECTION E
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MARTIMARE R., CYCALLAGHAN M., PARSONS J., PERCY C.,
EARSA A., SAUGUDES D., SHUMKERN R., SMALDON N., SMITH A.,
E., CALEN K., SULSTON J., THIERKY MIDS J., THOMAS K.,
VAUGUAN K., WALEKSTON R., WATSON A., WEINSTOCK L.,
HI KARLIAL K., BALLMAN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANN. THE ANDRESON N. BAYNES C. BERKS M. BONFIELD SONNEL M. CRAXTON M. SONNEL M. SERVE T. COOPER J. COULSON A. CRAXTON M. SERVE T. COOPER J. COULSON A. CRAXTON M. SERVE T. COOPER J. SERVE M. SE
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HERSE, HERBANK, GUBLI DATA BANKS
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Pred. No. 1.2c+93;
1; Mismatches (
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Q20792;
Q1-NOV-1996
Q1-NOV-1996
WILSON B., AINSCOUGH R., ANDERSON K., BAYNES C., KLEKS M., BONFIELD J.,
BURTON J., CONNELL M., COPSEY T., COUPER J., COULSON A., CRAXTON M.,
DEAR S., EU 7., EMPRIN R., FAVELLO A., FULTON L., CARDINER A., GREEN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAENORHABDITIS ELEGANS.
EUKARYOTA: METAZOA: NEMATODA;
                                                                                                                                                                         SEQUENCE FROM N.A MEDLINE: 94150718
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A MCMURRAY A.;
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SEQMENCE 450 AA; 50023 MW;
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PEAM: PE00105; zf-c4; 1.
RECEPTOR: TRANSCRIPTION REGULATION: DNA-BINDING: NUCLEAR PROTEIN:
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DEVELOPMENT 124:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIAW G.J., STEINGRIMSSON E., PIGNONI F., COUREY A.J., LENGYEL "Characterization of downstream elements in a Raf-1 pathway." PROC. NATL ACAD SCI U.S.A. 90:858-862(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 93157371.
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SURARFOIA: METAZJA: ARIHKUFUJA: IPACHEAIA: HENAFUJA: INSE
PIERKROTA: DIFFERA: FRACHEVIERA: MUSCUMUPPHA: EFHYLMOTINEA:
LMOSOPHILIDAE: DROSOPHILA:
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G1:JAN-1998 (TREMBLREL 05, LAST SEQUENCE OTHAIL)
G1-WW-1998 (TREMBLREL 08, LAST ANNUTATION UPPAIR)
TAILLESS PROTEIN.
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(TREMBLREL: 01, LAST SEQUENCE UPDATE)
(TREMBLREL: 08, LAST ANNOTATION UPDATE)
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R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, L.M.; Handelin, H.L.; Horsman, R. science 227, 268-275, 1987
A.Tille, Cloning of human minoral-modificated respirations and the control of human minoral-modificated respirations (AWA: Structural and A. Peference comber, A29513, MOID.87263386
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A.Fesidues: 1-33 CPAR.
A.Fesidues: 1-33 CPAR.
C:Comment: This peptide has antimicrobial activity.
C:Superfamily: ranalexin precursor; dermorphin precursor aminosterminal lowelos;
C:Keywords: disulfide bond: skin
F:27-33/Region: rana box motif
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N:Alternate names: aldosterone receptor
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B:TILLe: Antimicrobial peptides from the skin of a Karean Frod.
A:Reference number: PC2300
A:Accession PC2302
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C:Paio: 25-mob-1995 #moquonco_rovision 26-May-1995 #moxt_chindo (M-Apr-2008
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C.Keywords: disulfide bond: skib 
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Biophys Res Commun 205, 948-954, 1994
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N.Alternate nomes: graliee mortier protein, proline permease, proline transpurt protein
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A; Gone . .
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ArTitle: DNA sequence of the puth gene from Salmonella typhimurium and
A:Reterence number: $18229, MUID:98272423
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C:Superfamily: G surface protein
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A:Molecule type: DNA
A:Residues: 1-2718 <PRA>
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A:Title: Nuoleoidee sequence of the Paramecium A:Poforeono number: $17475. MTID-87060034
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C:Species. Paramecium primaurella
C:Dato: 31-Mar:1900 #aoqueno_necialmo 31 Mar:1989
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A:Residues: 1-984 /AREN
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F.2.06/Domain: transmembrane #status predicted <TM1>
F.4073/Domain: transmembrane #status predicted <TM2>
F.128.147/Domain: transmembrane #status predicted <TM2>
F.129.125/Domain: transmembrane #status predicted <TM3>
F.129.125/Domain: transmembrane #status predicted <TM5>
F.297.120/Pommin: transmembrane #status predicted <TM5>
F.297.120/Youndin: transmembrane #status predicted <TM8>
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F.297.120/Youndin: transmembrane #status predicted <TM8>
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F.293-255/Domain: transmembrane #status predicted TM05*
F.274-997/Domain: transmembrane #status predicted TM05*
F.377-392/Domain: transmembrane #status predicted TM08*
F.377-392/Domain: transmembrane #status predicted TM09*
F.397-122/Domain: transmembrane #status predicted TM09*
F.397-122/Domain: transmembrane #status predicted TM13*
F.458-447/Domain: transmembrane #status predicted TM13*
F.458-473/Domain: transmembrane #status predicted TM13*
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A;Accession: JC2382
A;Molecule type: DNA
A;Besidues: 1-494 HOS.
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N/Alternate names: proline permease
C:Species - Pseudomonas fluorescens
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R:HAbu, D. R: Myers, E.S.: Kent, C.R.: Maloy,
Mol. Gen. Genet. 213, 125-133, 1988
A.Title: Regulation of proline utilization in
A.Esteronce number 20 with MUICL29127131
A.Ruscession: S03816
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100.0%; Prod. No. 1 45+32;
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[001.0%; Prod. No. 1.16+02;
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Rizhou, Q.Y.: Li, C.; Glah, M.E.; Johnson, R.A.; Stilvs, G.L.: Givelii, T. Proc. Natl. Acad. Sci. U.S.A. 89, 7432-7436, 1992
A;Title: Molecular cluming and characterization of an adenosine receptor: the A: aden A:Beference number: A46152, MUID:93366475
A;Accession: A46152
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F)17-4/Domain: transmembrane #status predicted <TM3.
F)129-150/Domain: transmembrane #status predicted <TM3.
F)129-150/Domain: transmembrane #status predicted <TM5.
F)180-200/Domain: transmembrane #status predicted <TM5.
F)180-180/Binding site: Palmitate (Cys) (covalent) #status predicted
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Matches 5: Conserve
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ERS Lett 284, 155-160, 1991
A.Title. Molecular closing for novel potative 3-party be conjuditive; No. 100 to A.Peference number: S17177; MTID:91295122
A:Accession: S17177
   Ö
                                                                                                                                                                                                                                                                                   C;Superfamily: adenosine receptor Al C;Keywords: G protein coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                            A;Note: sequence inconsistent with the nucleotide translation A,Note: sequence extracted from NCRI backbone (NCBIN-11066)
                                                                                                                                                                                                                                                                                                                                                                                                                 A,Residues: 1-200-02807
A,Closs-references: 38 MM41720 NTH g200724, GTO g481272
A)Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A3 adenosine receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1943 #sequence_rovision 14-Nov-1444 #toxt_chunde 13-Sep-1998
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P.Eleischmann, E.D. Adams. M.D. White, O. Clayton, R.A., Kirkonsk, E.E., Konlawade 7. Georgyne, J.D., Scott, J., Shirley, R., Liu, E.T., Glodek, A., Kelley, J.M., Weldman Science 259, 496-512, July and C. Roman, M.C., Nguyan, D.T., Saudek, D.M., Rr Alauthors: Cotton, M.D., Uttarback, T.P., Hanna, M.C., Nguyan, D.T., Saudek, D.M., Rr V., Fraser, C.K., Smith, H.O.: Venter, J.Ç.

Affille: Whole geneame random sequencing and assembly of Facepophlius influenzae Ed

hypothetical protein WIC342 Hasmophilus influencas (Ettli: 84 PW30) C;Species: Hasmophilus influencas C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998 C;Accession: H64148

RESULT

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probable VMP kinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
C:Accession: E71484
R:Stephens PS - K91man, S : Lammel, C J : Fan, J : Marathe, R : Arawind, L : Mitchell,
submitted to GenBank, May 1998
A.Description, Genume sequence of an obligate intracellular pathogen of humans: Chlamydi
A:Reference number: A71460
A:Reference number: A71460
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A:Residues: 1245 ARN>
A:Resi
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100.0%, Score 26, DB 2; Longth 113;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0: Mismatches 0; Indels
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Self-response tertilisation: sperm surface protein:
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Example 4: Fig 5: 79pp: English.

Sperm Surface proteins or peptides stimulate an immune response to produce antibodies which block sperm-egg fusion and provide produce antibodies which block sperm egg fusion and provide proteins are the PH-2 and PH-
                        02-MAR-1995.
19-AUG-1994; U09395.
20-AUG-1993; US-110158.
(OKLA ) UNIV OKLAHOMA STATE
MCCYCT_RP, Pan J:
                                                                                                                                                                                                                                                                                                                                       R65216;
04-0CT-1995 (first entry)
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sperm surface proteins.
Sequence 275 AA:
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                                                                                                                                                                      WO9506118-A.
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WP1: 94-00 '200,001
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10-JUN-1993; U05640.
12-JUN-1992; US-897883.
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prodn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 STLSC
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95-106847/14
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Pred. No. 2.5e+02;
""-matches 0;
                                                                                                                                                                                                                                                                                       endothelial
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Best Local
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Matches S. Tonservative
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                                                                                                                                                                                                                                                                                                               DNA and protein sequence(s) for novel adenosine receptor, A3 - all recombinant vector contg the DNA, DNA probe(s), and cell culture transformed with the vector. Claim is figure 1, 29pp; English.
A3 adenosine receptors produced from cloned genes may be used to extrem compounds for A3 adenosine receptor activity, or for determining the amount of adenosine agonist or antagonist drug in solution. The DNA or its fragments may also be used as probes to determine tissue distribution of the receptors, to detect the placement of also gene or in EFEF to detect genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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Par A3 adence in receptor:
A3 adence in receptor is rewaited libertification agenist,
astrophist drug probe detection, genetic disorder; REIP
curification (separate to jib polymorphism
02-SEP-1996 (first entry)
Interferon gamma production inducer protein
Interferon gamma production inducer protein
Interferon gamma, inducer, IFNgamma; immunocompetent cell; antiviral;
antitumour, ant Septic, immunocepulatory; platejetinoreasing agent
therapy; proceeding, occeptions a commission, renal cancer; brain cancer
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disordors
                                                                        R92506 stundard, Protein; 157 AA R92506;
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Errs W. 24422;
Mismatches O. Indels
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7.20+02.
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PI cytotoxicity induces IFNgamma production in cytotoxicity of the invention. This protein is useful as an antiviral.
PI cytotoxicity of the protein cells and cytotoxicity and flately. Cytotoxylora actavinatum.
PI can be used for theating or preventing AIIS, original and cytotoxicity of the protein can also be used to induce IFNgamma production in cytotoxicity of cytotoxicity of the protein cells and when used with interlocking (IL-2) and tumour cytotoxicity of the protein (INF), may improve the effect of the cytotoxicity of the protein (INF), may improve the policy of the protein contains and production in production in protein which can then be putliced (it assayed)
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WFI; 95-070177/08.
N-PSDB; T92506.
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Mouse mature interferon-damma inducer protein.
Interferon-damma inducer protein: IFN-gamma: antiviral virunide:
antitumour: antibacterial: immunoregulator: adoptive immunothorapy:
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Kohno K. Kunikata T. Kurimoto M. Okamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUL-1995; 304906.
14-JUL-1994; JP-184162.
10-FEB-1995; JP-045057.
              (HAYR ) HAYASHIRARA SEIRUTSU KAGAKU
FUKUda S. Kobno K. Kusikata T. K.
Taniguchi M. Tanimato T. Tarigos K.
WTI: 96-252887/26.
N-PSDR T32403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using monoclonal antibodies. Sequence 157 AA;
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22-MAY-1996.
                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                               F99559;
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                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                  therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 STUSC
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interferor gamma productinducing polypoptido
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                                              Kalimoto M,
Table S;
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1.65+02;
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A 1.11 by min
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1.14 box 1.15
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ion 19
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9,555. df.
77, 676.
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                                                undering tactor 2 (1318 2) 81401 cariabt.
Inductor tactor 2: 101E-2: leadscyto: lymphocyto:
iteration, differentiation, materation, tissue d
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100.0%; Pred. R5; 1.60.02;
150. %; Mismathles 0;
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Pred. No. 1.6
Mismatches
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-hes 0;
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Query Match

Best Local Similarity
Thiches 5; Conserv
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W09724441-Al.
10-JUL-1997.
20-UEC-1997. U20432.
29-UEC-1995. US-580667.
(INCY-) INCYTE PHARM INC.
Cocks RG. Coleman P. Haw
Claim 1: Rage 46; 60pp; English.

Claim 1: Rage 46; 160pp; English.

(IGIF-2) A: IGIF-2 variant (W3187); and an IGIF variant (W22049).

Which may be an alternate transcript, also exist Probes derived from the world, acid sequences can be used to public; the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2, such as antibodies, antagons's or other that increat with IGIF-2, such as antibodies, antagons's or other than increat with IGIF-2, such as antibodies, antagons's or other than increat with IGIF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein sequence represents an interieron wamma inducing factor: (ICIF 2) wariant, identified from a liver cDNA library. This sequence differs from ICIF-2 identified from a Tlymphocyte cDNA library (W2204) in that amino acid 140 is found to be changed from Ard to lie. A second variant, W2204, the Arst Note Protein defined from Ard to lie. A second sequences can be used to quantify the expression of ICIF-2 in conditions that are associated with inflammation or aborrant expression of ICIF-2. The protein can be used to screen for compounds that inflam the protein can be used to screen for compounds that inflam (expectable) riberyres or actions a satisfactor of TCIF 2 expression of expectable protein can also be used to diagnose, prevent or treat BiF 2 induction of proliferation, differentiation or maturation of treat BiF 2 induction of proliferation, differentiation or maturation of the options.
                                                                                                                                                                                                                                                                                    with inflammation Claim 1: Page 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interferon gamma inducing factor:2 (IGIF:2) protein.
Interferon gamma inducing factor:2, TGIF 2, leading to laphoryte;
inflammation; proliferation; differentiation; maturation; tissue damage.
                                                                                                                                                                                                                                                                                                                                                      Novel interferon gamma inducing factor 2— used to screen for companyeds to diagrass, treat or present tissue damage associated
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-36:677/33.
N-PSDB; T74987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: This sequence does not appear in the specifications it been made by modifying the ISTE'S sequence presented in W20047. Sequence 193 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel interferon gamma inducing factor:2 - used to screen to remposed to diagnose, treat or prevent tissue damage asser-
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20 DEC 1996; U20432.
29-DEC-1995; US-580667
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Cooks RG. Coleman P. H
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Pred. No. 1.9e+02:
Prematches 0:
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W27056
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Best Local
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The present sequence represents a novel protein from mouse liver cells, which induces interferon-gamma (IFN gamma) production in immunocompetent cells. This protein enhances cytotoxicity of killer cells and induces their formation. It is used as an antioncotic agent for antitumour immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and in the represent of the line including anti-AIDS) or antibacterial agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in the freatment of atopic or immune system diseases, e.g. asthma, hayferer or rheumatism. When formulated with interleukin-3, it is also sed to treat leab parents and tother parents and tother cancers. When used in antitumour immunotherapy of louksomia and other cancers. When used in antitumour immunotherapy this novel protein significantly improves the immunotherapy title feet of interleukin-2 (II-2), compared with use of II-2 alone, either when administered to the patient (before administration of the system of the modium in which calls (intended for return to the patient) are being grown sequence 157 AA:
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Wouse Interferon-gamma inducer protein.
Interferon-gamma, IFN gamma; antiviral; antioncotic; radiotherapy;
Immunoregulatory, antitumour agent; chemotherapy; leukopaenia;
thrimbiosycepaenia, immunocompetent cell, asthma, hayfever,
rheumatism, interleukin, killer cell
W27056 stundard, peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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Similarity 100.0%;
5, Conservative 0,
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larity 100.0%;
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Pred No 1 4e+02;
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                                                                                                                                                                                                                                                                                           Score 26; DB 1;
Pred No 1 Ke+02;
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PR MARIS 97-448633/4]

Fix Kricks r. Stadler B.

PR MARIS 97-448633/4]

Fix Kricks r. Stadler B.

Pr Wovel minority (5)

Fix vaccines against 135 mediate builth allergy

Recording against 135 mediate builth.

Pr vaccines against 135 mediate builth.

Pr vaccines against 135 mediate builth the terminal cysteine residues) was

CC This peptide sessuence (Without the terminal cysteine residues) was

CC displayed by RSW17 mimeotope phages. The peptide was synthesised

CC with the additional cysteine residues for circularisation. The

Peptide was used in a new immunogenic molecule for raccination against

CC and treatment of allery. The immunogenic molecule comprises at least

CC and treatment of allery. The immunogenic molecule comprises at least

CC and treatment of allery. The monoclonal anti-human Ige

CC immunoglobulin E (IgE) recognised by the monoclonal anti-human IgE

CC antibody 85W17 and a molecy capable of eliciting an immune response

CC against the peptide. The peptide is used in the preparation of vaccines

CC against an IgE-mediated disease, especially allergy. The molecules can

CC cell/basephil triggering by blocking lugger cystlos in applicable to 

CC cell/basephil triggering by blocking lugger cystlos in applicable to 

CC cell/basephil triggering by blocking lugger cystlos in applicable to 

CC cell/basephil triggering by blocking lugger of properties. The molecules 

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CC cell/basephil triggering by blocking lugger of properties of properties.
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01-APR 1998 (first ontry)
01-APR 1998 (first ontry)
Exptide Assaular as #9 displayed by BSW17 mimostipe phages.
Peptide immunogen, varcination, alleggy, epitope, IgE, immune response:
immunoglobulin E. antibely BSW17, attple dermatitie, BSW17 simestope;
antibody: mast cell; bas pull, immunisation, mimostope phage: circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY 1998 (first entry)
Amino acid sequence of numer interleukin-1-gamma.
Interleukin-1-gamma, It-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, It-1-gamma, III-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, II-1-gamma, II-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, II-1-gamma, II-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, II-1-gamma, II-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, II-1-gamma, II-1-gamma, meuse, cytekine, ISIF, literiferon-Tamma:
Interleukin-1-gamma, II-1-gamma, II-1
kegior
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01-MAR-1996; GB-004412
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88
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                                                                                       "beta-5 region"
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Actualist : burns interloukin-l-gamma - used for treating seminologic disorders coused by burna Hill-gamma (IL-1-gamma). Series for the 45% of the problem interleukin-l-gamma (IL-1-gamma). The present sequence represents burnar interleukin-l-gamma (IL-1-gamma). The problem is present sequence by the following containing the sequence represents burnar interleum gamma. Human IL-1-gamma intersection camma is the sequence of the following containing the sequence of the following containing a sequence of the following containing a sequence of the following containing a sequence of the following containing and the sequence of the following containing a sequence of the following containing the sequence of the following containing the sequence of the following containing the following containing the following containing the following the following containing the following containing the following containing the following containing containing the following containing the following containing containing the following the following containing containing the following containing containing containing containing the following containing c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived is analysis of the total soure distribution.

SUMMARIES

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ALIGNMENTS

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SEQUENCE OF 149-1896 FROM N.A. REDILINE, 87049597. TLAKAPAN 1. HAND FOULTH-TIADARAS M., AVILA E., NUSSBAUM A.L., NICOLOGI E., ZANNIS VII.; "Completending TNA delived structure of the united terminal denain of hamon epoliphys TNA delived structure of the messenger RNA transcript.": Eldermiser PV 20.5:01 1507(156)	Ol-NOV-1996 (TREMBLEEL 01, CREALED) Ol-NOV-1996 (TREMBLEEL 02, LAST SEQUENCE UPDAIE) Ul-NUV-1996 (TREMBLEEL 08, LAST ANNOTATION OPDATE) APOLIFOPROTEIN BLU. APOB. HOMO SAPIENS (HUMAN). ETYARFOTA MYLANA, HIPPATAN VERTEBBATA, MAIMALIA, SUTHOLIA, ERIMATES; CATARRETIA: HOMINIDAE: HOMO.	315 S1 316 S1 13787	1 1 1 1 1 1 1 1 1 1	The 100 0x. Score were by 1: similarity include Fred. No. J. Serv. 5. Conservative 2. Mismatches	(2) SEQUENCE FROM N.A. MIPS: MIPS: STREMITTED (TUI 1006) TO EMPLITEMBANKITED TAKE FAMES. SEMBL: 274121; E253014) SEQUENCE	(1) SEQUENCE FROM N.A. WEDLER E., SCHARFE M.; SUBMITTES (TOL-1995) TO EMPLYSENBARK, DOBJ DATA BANKS.	OU 434: 01-NOV-1996 (TREMELREL 01, CREATED) 01-NOV-1996 (TREMELREL 01, LAST SEGGENCE UPDATE) 01-NOV-1996 (TREMELREL 01, LAST ANNOTATION UPDATE) SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). SACCHAROMYCES ASCOMYCCIA: HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES.	T 1 472454 PRELIMINARY: PRT; 984 AA.

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SEQUENCE FROM N.A.

MEDLINE, 94150718, ANDERSON K. BAYNES C. BERKS M., BONFIELL I.

BUSION F. AINSONIGH F., ANDERSON K., BAYNES C. BERKS M., BONFIELL I.

BUSION J. CONNELL M. COPSEY I., COOPER J., COULSON A., CHAXTIN M.,

BUSION J., CONNELL M. COPSEY I., COOPER J., COULSON A., CHAXTIN M.,

FLAKE S. TH., LIGHTLIN F. FAVELL A., FULTON I., JANGALA A., CHAXTIN M.,

KIPSTEN J., LAISTER N., LATRELILE P., LIGHTNING J., LIGHTNING J., HOLD T.,

KIPSTEN J., LAISTER N., LATRELILE P., LIGHTNING J., HOLD T.,

MOMINDRAY A. MORTIMORE B., O'CALLAGHAN M., PARS'NS J., PERCY C.,

MOMINDRAY A., MORTIMORE B., O'CALLAGHAN M., PARS'NS J., PERCY C.,

SONNHAMMER F., STADEN W., SULSTON R., WATSON A., WEINSTOCK I.,

WILKINSON SEPOAT J., WOHLDMAN P.,

WILKINSON SEPOAT J., WOHLDMAN P.,
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093238: 01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDAIE)
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NATURE 368:32-38(1994)
EMBL: Z78415: EZ59012:
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CAENOPHABITTIS ELEGANS
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O5, LAST SEQUENCE UPDATE;

O8, LAST ANN/TAITON UPDA(E)
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ETTATEAT
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SOB PRODUCTION OF CONTRACT CON
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BURION J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
BURION J., DURBLE M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
DURBL N., COPER M., FULTON L., JONES M., KERSHAW J.,
HAWKINS I., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
MCMURRAY A., MOETIMUHY B., G. CALLAGHAN M., FARSONS J., PEPCY G.,
MCMURRAY A., MOETIMUHY B., G., SHOWNKEEN R., SMALDON N., SMITH A.,
RIPKEN L., POOPER A. SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
SONNHAMMER E., STADEN P., STILTON T., THIERY-MIEG J., THOMAS K.,
VAUDIN M., VAUGHAN K., WHATERSTON R., WATSON A., WEINSTOCK L.,
WILKINSCHIETEAT J., WCHICHMAN P.
WILKINSCHIETEAT J., WCHICHMAN P.
"2.2 M. of Contiguous muclectide sequence from chromosome III of C.
"2.2 M. of Contiguous muclectide sequence from chromosome III of C.
"2.2 M. of Contiguous muclectide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
MEDLINE, 94150719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHABUITINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2:
PAULEY A., MAGGI I HARPER M.:
SUBMITTED (ANG-1997) TO EMBL/JUNKANK/UDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBJUTNIE (JÚL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
TMB: AFOLUGIE, JES15672, ...
SEQUENTE 332 AA. 37377 MW. F256779D CPC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATERSION R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN BRISTOI NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATimes signate series.
                                                                                                                                                                                                                                                                                               WILSON R. JAINSCOUGH P., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON T., CONHELL M., COPSEY T., COOPER T., COULSON A., CRANTON M., BURTON T., CONHELL M., COPSEY T., COOPER T., COULSON A., CRANTON M., BURTON T., CONHEN M., CRESHAW J., CHARLES T., COLLEGE M., CARDINER M., CARSHAW J., CHARLES M., LICHTON L., JONES M., KERSHAW J., KINSTEN T., LICHTON L., JONES M., KERSHAW J., KINSTER N., LICHTON L., JONES M., LICHTON C., KINSTER N., LICHTON M., TAPSONS J., LICHTON C., MCMURRAY A., MORTIMAKE E., COLLAGRAM M., FARSON M., SHOWINKEEN R., SMALDON N., SMITH A., SOUNIMANIE E., CRAICEN F., STUSTON F., WATSON A., WEINSTOCK L., VAUGIN M., VAUGHAN E., WAIEPSTON P., WATSON A., WEINSTOCK L., VAUGIN M., VAUGHAN E., WAIEPSTON P., WATSON A., WEINSTOCK L., WAIEPSTON P., WAIEPSTON P., WATSON A., WEINSTOCK L., WAIEPSTON P., WATSON A., WEINSTOCK L., WAIEPSTON P., WATSON A., WEINSTOCK L., WAIEPSTON P., WAIEPSTON P., WATSON A., WEINSTOCK L., WAIEPSTON P., WAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA, METAZOA: NEMATODA; SECEPNENTEA: RHABDITIA; RHABDITIDA;
EHAECITIMA, FHAROITOTDEA: PHARDITIDAE: PELODERINAE: CARNORHARDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N A
MEDITNE: 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 STLSC 234
                                                   NATURE 368-32-38(1994).

-:- SUBSCILLULAR HOUGHIN. INTESPAL MEMBRANE PROTEIN (RY SIMILARITY).

-:- SIMILARITY PRIONGS TO THE LIGAND-GARED HONIC CHANNELS PAMILY.

EMBL: 297807 - E1186516: -.
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hos 5: Conservative
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RHADDITOIDEA, RHAEDITIRAE; PELICEPINAE: CAENORHAEDITIS
    PS00236; NEUROTR_TON_CHANNEL;
                                                                                                                                                                                                                                                              contiguous nucleotide sequence from chromosome III of \boldsymbol{\psi}
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100.0%; prod No.
3: Mismatches
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05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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POSISYNALIIC MEMBEANE, ICHIO CHANNEL: GLYGUPECIBIN, IRANGMEMBEANE
SEQUENCE 545 AA, CLECI MW. 26207FTS CF-30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  047551 PRELIMINARY: PRT: 489 AA. 047551; 01.NOV-1996 (TREMBLREL 01, CREATED) 01.NOV-1996 (TREMBLREL 01, LAST SHOUENCE UPDATE) 01.NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                    047552;
047552;
01-NOV-1906
01-NOV-1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROLINE PERMEASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 489
SEQUENCE 489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evolutionary denotics of the proline permease dene (putP) and the control region of the proline utilization operon in populations of Salmonella and Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTER!A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 STLSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00456; NA_SOLUT_SYMP_1; PROSITE; PS00457; NA_SOLUT_SYMP_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. BACTERIOL. 174:6886-6895(1992).
EMBL; L01133; G147437; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NELSON K., SELANDER R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 93015751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00474; SSF;
        "Evolutionary genetics of the proline permease gene (putF) and the control region of the proline utilization operon in populations of salmonella and Escherichia coli.";
3. BAJIESTA. 174.6881-C227 (1992).
EMBL. L01122: G1474443; ...
                                                                                                                                                                                         01-NOV-1998
                                                                                                                                       BACTEFIA, FECTERBACTEFIA
                                                                                                                                                  ESCHEDICHTA COLI
                                                                                                                                                                              PROLINE PERMEASE (FRAGMENT)
PROSITE: PS00456; NA_SOLUT_SYMP_1:
                                                                                                                                                                                                                                                                                                         340 SILSC 344
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                                                                                   SEQUENCE PROM N A. MEDLINE; 93015751.
                                                                                                                            ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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5, Conserv
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                                                                          SELANDER R K.,
                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; conservative 0
                                                                                                                                                                                          (IPEMBLFEL
                                                                                                                                                                                                     (TREMBLREL)
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                                                                                                                                           CAMMA SUBDIVISION: ENTEROPHOLIPRIACEAE
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                                                                                                                                                                                                                      CREATED)
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Pred No. 1.8e+02
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                                                                                                                                                                                                        SEQUENCE UPDATE)
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Rest Caral Casilatity
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55-77-56
"For latic at a condition of the proline permease gene (putp) and the sale telephon of the proline utilization operon in populations of the sale utility to the above the coling the sale of the sale 
                                                                                                                             NEES A K
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                                                                                                                                                                                                         HANTIERIA: OF THE HARDERIA: ALPHA SUBDIVISION: RICKETTSIALES; RICKETTSIA, OF TRAINING BURNETTSIA.
                                                                                                                                                                                                                                                                 KITEISIA
                                                                                                                                                                                                                                                                                            OF NOV-19 OF (TREMBUREL, 01, CREATED)
OF NOV-19 OF TREMBUREL, 01, LAST SEQUENCE UPDATE)
OF NOV-14 OF TREMBUREL, 08, LAST ANNOTATION UPDATE)
FROM THE FERMEARY (FRAMBURY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100,0%: Scote 26: D8 9, 37y 100.0%: Pred. No. 1.8e+02: 0: Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
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100.0%: Pred. No. 1.8e+02;
tivo 9: Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPREE WM: 2FARGA8B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REALED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    489 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ladels
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RESULT 13
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Best Local Similarity
Thehes 5; Conserve
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Best Local :
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"Evolutionary genetics of the proline permease game (puth) and the control region of the proline utilization operon in populations of Salmonella and Escherichia coli.";
                                                                                                                                           Q54979 PRELIMINARY: PRT; 489 AA.
U54979;
01-NOV-1995 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
                                        SEQUENCE FROM N.A.
MEDLINE; 93015751.
NELSON K., SELANDER R.K.;
                                                                                               BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION; ENTEROKACTERIACEAE:
                                                                                                                                  PUTP
                                                                                                                                                                                                                                                                                                                                                                                         "Frolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of Talanonella and Escherichia coli.";

T. BACTEPYOL. 174 FRRC.5895(1592);
EMBL: D0136; G154292;
PROSITE: PS00455; NA_SOLUT_SYMP_1;
PROSITE: PS00457, NA_SOLUT_SYMP_2;
PROMITE: PS00457; NS_SE;;
PROMITE: PS00457; NS_SE;;
                                                                                            SALMONELLA
                                                                                                                  SALMONELLA SP
                                                                                                                                          PROLINE PERMEASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                               SECHENCE
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054978;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                  340 STLSC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFLSON K., SELANDER R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STPAIN-S2985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA;
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PROSITE: PS00457: NA_SOLUT_SYMP_2;
PEAM: PF00474: SSF; 1.
NON_TER 489 489
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SEQUENCE 489 AA;
                                                                                                                                                                                                                                                                                        1 STLSC
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hes 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEOBACTERIA; GAMMA SUPDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                        U
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489 AA; 52857 MW,
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                       Score 26; DB 9;
Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                      4883A88B CKC32;
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                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of salmonella and Escherichia coll.";

J. BROTERIOL 174:6886-6895(1992).

EMBI: 101129: 0154296;

EMBI: 101129: 0154296;

EMBI: PS04455; NA_SOLUT_SYMP_1: 1.

PROSITE: PS04557: NA_SOLUT_SYMP_2: 1

PEAM: PF00474; SSE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. BACIERIO: 17:102800000(1092);

EMBL: 101137: 0154291;

PROSIIB: FSC0056: NA_SCLU: SYMP_1;

FROSIE: FSC0457: NA_SCLU: SYME_2;
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MEDLINE; 93015751.
NFISON K , SELANDE
                                                                                                                                                                                                                                                                                                                                                                                      Q54981 PRELIMINAPY: PPT: 489 AA Q54981; Q54981; Q1-NOV-1996 (TREMBLREL 01, CARATER) Q1-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE) Q1-NOV-1998 (TREMBLREL 09, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O1-NOV-1996 (TREMBLEEL O1, CHEATED)
O1-NOV-1996 (TREMBLEEL OB, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLEEL OB, LAST ANNOTATION UPDATE)
PROLINE PERMEASE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054980;
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                                        STRAIN=S2003;
MEDLINE; 93015751
                                                                                                                                                                                                                                                                            SALMONELLA SP.
                                                                                                                                                                                                                                                                                                                                                          PROLINE PERMEASE (FRAGMENT).
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                       SALMONELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 STLSC 344
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5; Conserv
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5: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 AA.
                                                                                                                                                                                                                                            PROTEOBACIERIA: SAMMA SURDIVISION, ENTEROBACTERIACEAE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 A.A.
                SELANDER R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 9; ;
Pred. No. 1 8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 489
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Query Match
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Search completed. June 12, Job time: 170 sec
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BACTEFFOL 174:698--848(1942)
EMBL: 101139: G154298.
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SECTENCE 489 AA:
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PPOSITE: FS00457, NA_SOLUT_SYMP_2 1.
PFAM; PF00474; SSF; 1
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                                                                                                                                                                                                                                                                                                                         P38557 homo sapien
Q14116 homo sapien
P70380 mus musculu
Q19073 sus scrofa
P70380 rattus norv
P1610a homo sapien
P08235 homo sapien
P44650 haemophilus
P41383 schiaosachia
P54351 dxosophila
P54351 dxosophila
P71147 escherichia
P10502 salmonolla t
P16782 buman sytom
P23269 african sytom
P23269 sarnian sytom
P23835 sarcharumyc
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P39533 saccharomyc
QC5159 brachydanio
P13837 paramecium
   P05622
P24386
P80956
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P42542
F43920
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-1- SIMILARITY: BELONGS TO FAMILY I OF G-
EMBL, X59249; G56308; -.
EMBL, X93219; E213918; -.
EMBL, X93219; E213918; -.
FIR; A6152; A6152;
G5F1B, G6E_2377;
G7FDB, G6E_2373; -.
G7FDB, G6E_2373; -.
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MEDLINE; 92366475
TEANSMEM
TEANSMEM
DOMAIN
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ADORA3.
RAITUS NORVEGICUS (BAT).
EUKAFYTTA, METATIA, THOFFTATA, 1
                                                                                                                             GCRDB; GCR_1262; -
                                                                                                                                                                                                                                                                                                                   MEDLINE: 91285122.
MEYERHOF W., MUEILL
FEBS LETT. 284.155
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Charlet Esceptie, Transmembrane, Ginciprotein
IN, PALMITATE, ALTERNATIVE SPLICING.
IN, PALMITATE, ALTERNATIVE SPLICING.
1 16
EXTRACELLULAR (POTENTIAL).
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I US A. 89:7432-7436(1992).
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       28. (REACH)
28. LAST SHOURNCE UPDATE)
6. LAST ANNOTATION UPDATE)
6. LAST ANNOTATION UPDATE)
6. MSE PROTEIN 2 (EDR.) (RECY.28 PROTEIN) (REW.20)
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| I. -> N (IN REF. 1).
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RON-SULFUR (4FE-4S) (BY SIMILARITY)
RON-SULFUR (4FE-4S) (BY SIMILARITY)
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Best Local Similarity
Watches 5 Conser
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OXTORY E., JOWEIT I.:

NUCLEIC ACTUS RES. 21:1087-1095(1993).

--- FUNCTION: SEQUENCE SPECIFIC DNA BINDING TRANSCRIPTION FACTOR.

FUNCS TO INC. SECUENCE UNA SITES LOCATED IN THE PROMOTER REGION.
                                                                                          MEDLINE; 87060934.

PRAIT A., KAIDAM., CARON F., MEYER E.:
J. MOL. BIOL. 189.47-60(1986).

-!- FUNCTION: THIS PROTEIN IS THE SURFACE ANTIGEN: 4
                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-AUG-1990 (PEL. 15, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRACHYDANIO KERIO (ZEBKAFISH) (ZEBKA DANIO).
EUKARYOTA: METAPOA: CHORDATA: VERTERRATA: DISCES: CNCLEOSTEMATA:
OSTEICHTHYRS: ACTINOPTERYST! CYPRINIFORMES.
ANTIGEN OF PARAMECTUM PRIMAURELIA.

11- SUBCELLULAR LOCATION: AITACHED TO THE MEMBRANE BY A OPI-ANCHOR.

11- TIT HAR INTERNAL HOMOLOGIPS AND A HIGHLY PERIOD CONTAINING 8

37 PERIODS OF ABOUT 75 RESIDUES, EACH PERIOD CONTAINING 8
                                                                                                                                                                                                                                                        PARAMECIUM PRIMAURELIA.
EUKARYOTA: PROTOZOA: CILIÓPHOKA: CILIATA: HOLOTE:CHA: HYMENOSTOMAITEA
                                                                                                                                                                                            STRAIN-156
                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                     P13837
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                                                                                                                                                                                                                                                                                                                                        156G SURFACE PROTEIN PRECURSOR
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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Pred. No. 66;
Mismatches
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GAE2_RANRU
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Best Tonal S
  GAE3_RANRU
P80797;
01-NCV 1395;
E1-NOV-1995;
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P80396;
01-NOV-1995
01-NOV-1995
01-NOV-1997
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PARK T M TONG T.E. IFF B T.

BIOCHEM. BITPHYS. RES. COMMUN. 205:948-954(1994).

-!- FUNCTION. HAS A NON-HEMOLYTIC ACTIVITY HAS A BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE HACTERIA, FUNGI AND PROTOZOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMPHIBIAN SKIN: ANTIBIOTIC. DISULFID 27 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: SECRETED
-!- TISSEE SEPTIFICITY SKIN
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PIR; A23475; A23475.
HSSP: P06620; lina.
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SIMILAFITY: 98% TO THE ALLELIC FORM 168G PROTEIN (P17053) IN
PERIODIC STRUCTURE AND 80% IN VARIABLE DOMAIN IN THE MIDDLE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY
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Harity 100
Opractivative
(REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
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                                                                                    STANDARD;
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(3, f3, f3
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LAST SEC
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ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                            1566 SURFACE PROTEIN
37 X 75 AA APPROXIMATE REPEATS
89% TO FARAMEDIUM TETRAURELIA /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
96F2A97A CRC32
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Pred No 3 5e+02;
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Best Local :
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            JONES M. 1. DAVEY P.M. APLIN H. AFFARA N.A.)

JONES M. 1. DAVEY P.M. APLIN H. AFFARA N.A.)

GRACHICS 29:796-800(1095).

11- EUNCTION: INVOLVED IN SPERM-FGG ADHESION. UPON FERTILIZATION SPERM MOST FIRST PENETRATE A LAYER OF CONDUCTS. THAT STERROUNGS THE FOR SEFTCHE FRACHING THE ZONA PELLUCIDA. THE COMMINIOS CELLS AFE EMBEDDED IN A MATRIX CONTAINING HYALLTRONIC ACID WHICH IS SHAMED PRICE TO CAUGATION. THIS SECIET NAIDS IN PRETENTATING THE LAYER OF CUMULUS CELLS BY DIGESTING HYALURONIC ACID.

ACID. ACCID. BEIA-1-GUOCOSAMINE AND D-GLUCUFONATE RESIDUES IN NAIDS TO ACCID. BEIA-1-GUOCOSAMINE AND D-GLUCUFONATE RESIDUES IN NAIDS TO ACCID. BEIA-1-GUOCOSAMINE AND D-GLUCUFONATE RESIDUES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYAI_HOMAN STANDARD: PRI: 509 AA. P88567; P88567; P98567; P98567; P98567; P98567; P98567; P98567; P98567; P98567; P98567; P98677; P986
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                                                                                                                                                                                                                                                                                                                                                                          FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN)
FURAFYSTA, METARSA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SPERM ADHESION MOLECULE 1). SPAM1 OR HYAL1 OR HE20.
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BUKASYMIA: MEINIUA, IBIELATA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAEGURIN-3
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                                                                                                                                                                                                                                                                                 MEULLNE
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Pp 10071-10075(1993).
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T.-19++ (REL. 36, LAST ANNOTATION UPDATE)
-CEUKIT 13 FEEDINGOK (IL-18) (INTEREGON-GAMMA INDUCTOR PACTOR)
GAMMA UNDUCTAL FACTOR) (INTEREGUKIN-1 GAMMA) (IL 1 GAMMA).
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THE TOTAL TO EMBLICIAL MANKED LATA HANKS
R. ACTIMENTS NATURAL KILLER CELL ACTIVITY IN SPIEEN CELLS
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KURST K., MIPANISE M., FUJII M., TORIGOE
IKEDA M., OKAMURA H., KURIMOTO M.,
156.1274 4279(1906).
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Score.
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019073;
15-JUL-1998 (PEL 36, CREATED)
15-JUL-1998 (REL 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)
INTERLEUKIN-18 PRECUPSOF (IL 18) (INTERLEUKIN-18 PRECUPSOF (IL 18) (INTERLEUKIN-18)
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OKAMURA H., TSHIHI H., KUMATSU F., YUTSUDO M., HAKURA A.,

TANIMOTO T., TORIGOE K., OKURA T., NUKADA Y., HATTORI K.,

AKITA K., NAMBA M., TANABE F., KONISHI K., FUKULA S., KORIMOTO M.:

OATURE 378:88-91(1995).
                                                                                                                                             SUS SCROFA (PIG).
FUKARYOTA METACOA.
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FOSS D.L , MURTAUGH M.P.;
                                      SEQUENCE FROM N.A
                                                                                                              EUTHERIA; ARTIODACTYLA
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EUKARYOTA: METAZOA: C
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTERLEUKIN-18 PRECURSOR (II-18) (INTERFEREN-SAMMA INDUCING FACTOR) (INTERFERENTIAL SAMMA) (IL-1 GAMMA).
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U66244; G1561736;
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Pred. No. 34;
                                                                                                                                         VERTEBRATA, TETRARIDA, MAMMALIA
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Best Local :
OJU AA.

ULTAPP-1990 (PEU 14 OPFATED)

01-AUG-1990 (PEU 15, LAST SEQUENCE OPPATE)

01-NOV-1997 (PEU 35, LAST ANNOCAZION UPDATE)

P-SELECTIN PRECUESOR (CRANDE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)

(TOTAL) (LEUK-TIE ENW-CHHAITAL CELL ADHESION M-LECULE 5) (LECAM3).

SELP OK GMRP.

HOMO SARIENS (HUMAN)
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MEDLINE: 97150962.

MEDLINE: 97150962.

TINTE G., SON J.H., TOH T.H.;

J. BYOL CHEM. 270120961203712097)

-1- FUNCTION: ANDMONTS NATURAL WITLES FELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTESEFFON GAMMA PROPROTION IN THELPER TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILIB_BAT STANDARD. PRT. 194 AA. 19755: 197637; 197637; 197755: 197755: 197755: 197755: 197755: 197755: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 19775: 1977
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-:- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLBEN CELLS
AND STREMITATES INTERFERON GAMMA PRODUCTION IN THELPER TYPE I
CELLS (BY SIMILARITY).
                                                                                                                                                                                                                    HUMAN
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EURAPPOTA METATOA, OHOPPATA, VEPTEPPAIA, IEIPAPOUA, MAMMALIA.
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MISSING (IN ISOFORM ALPHA)
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Pred No. 34
5; Migmatohas
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PROTEIN SCI 2:1798:1810(1993)

-1- FUNCTION: CA(2+)-FFFFENCENT RECEPTOR FOR MYELOIN
10 'ARECHYDEATES ... NEUTROPHIIS AND MONOCYTES. T
RECOGNIZED IS STALY:-LEWIS X.
                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00022; EGE_1; 1.
PS003ITE: PS01866; EGE_2; 1.
PR00811E: PS000419; C_TYPE_LECTIN_1; 1
PR0811E: PS00041; C_TYPE_LECTIN_2; 1.
CELL ADHESION; TPANKEMERANE; GIVPOPROJEIN; EGF LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCÉRLUTAR LOCATION. TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANGUSES (* FLATELETS AND WRIBEL-FALALE BOUTES OF EMPOTHELIAL CELLS CPPN CELL.
ACTIVATION BY AGONISTS, F-SELECTIN IS TRANSPORTED RAPHOLY TO THE CELL SURFACE.
-!- SIMILARITY: TOO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 POP-LIKE DOMAIN.
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FREEDMAN S.J., SA
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STRUCTURE BY NMR OF 160-199
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JOHNSTON G.I., COV
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EXTRACELLULAR (POTENTIAL)
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SHANN D. S. EVANS K.M.:

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190 0%; Mismatches
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01-N0Y-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPI
01-NOY-1995 (REL 32, LAST ANNOTATION 0)
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-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL: M16801; G307166; -.
EMBL: M29513; A29513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENTER J.C.;
SCIENCE 269:496-512(1995)
-1- FUNCTION: INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEPLAVAGE A P RUIT C T TOMR T -P DOUGHERT B.A. MERRICK J.M.
MCKERNEY K SUTTON G FITTHIGH W FIELDS C.A. GORAYNE J.D.,
SCOTT J D. SHIBLEY B. LIU L.-I. GLODEK A. KELLEY J.M.
WEIDMAN J.F. PHILLIPS C.A. SPRIGGS T. HEDBLOM E., O'TICN M.D.,
WEIDMAN J.F. SHIBLEY B. LUU L.-I. GLODEK A. GLODEK O. W. SHANDON P.C.
TITEBHACK T P, HANNA M C, NGUYEN D T, SAUDEK O. M. SHANDON P.C.
FRING L.D. FRITCHAAN J. F. FIHRMANN T L. GEOGHADEN N.S. M.
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HSSP; P06536; 1GDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNEHM C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE: 95350630;
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PROKARYOTA: GEACILICUIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: INVOLVED IN ELECTRON TRANSFER
-1- SIMILARITY: THE IFON-SULFIR CENTERS ARE
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PASTEURELLACEAE
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SUBMITTED (FEB-1996) TO EMBL/GENBANK/DIAD DATA BANKS.

-!- SUBMITTED (FEB-1996) TO EMBL/GENBANK/DIAD DATA BANKS.

-!- SUBMITTED (FEB-1996) TO PARTITION AND ESSENTIAL FOR VIABILITY.

-!- SUBMITTED FOOTHING NUCLEAR (POTENTIAL).

-!- SUBMILARITY: BELONGS TO THE MCM FAMILY.

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GenGule vergion 4.5

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CM protein - protein search using sw model

Run on:

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95.815 Million cell updates/sec

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Sequence:

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SUMMARIES

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ALIGNMENTS

Oppossed II I proteins are involved in the inflammatory responses being identification. Ils. Comment: This protein lacks a conventional signal sequence for protein export of void form of interleukin-lalpha, sullke interleukin-libera, is fully active. C.Sapertamily, interleukin-lalpha, sullke interleukin-libera, is fully active. C.Sapertamily, interleukin-lalpha, inflammation, liper telm. North-liber cac from our systemation interleukin lalpha #status predicted F.18-279/Ernding site, myristatte (bys) (covalent) #status predicted	RESULT 2 \$10532 interlewkin-1 alpha precursor - pig interlewkin-1 alpha precursor - pig N.Alternate dames, hematopolectic1, IL-1 alpha C.Species: Sus scrofa domestica (domestic pig) N.C.Eath 10:Fnh-1395 #shquareline(slot 12:Nur 1395 #th-t_line at 17:Nur-1397 C.Accession, \$10532 F.Maliszewski, or Pr. Brashaw R.P. Schoenborn, M.A. Withan, I.F. Baker, P.E. Nucleic Acids Res. 18, 4282, 1890 A.Title Forcine IL-1 alpha cDNA ducleutide sequence. A.Feference damber: Sit532 A.Scassion: \$10532 A.Status, preliminary A.Molecule type: mANIA A.Pest33es; 1:20 - MANIA A.Pest33es; 1:20 - MANIA A.Couss: reformica, EMBL.NSC331, NIE-31987; FID-31989 T.Coumment Fillows by artivated maniphass, the II-1 grateful sithulate thymos	62 VILSVEGENISTISGENERISERENNEERINKIERSTITTIEFSVEGHENEMEERSVE 1 63 VILSVEGENISTISGENERISERENNEERINEERINEERINGEERSVE 1 64 VILSVEGENISTISGENERISERENNEERINEERINGEERINGEERSVE 1 101 3VILAGERENGERINETISERENNETISTITTIEFSUMEVEGH NEMEERSLYE 1 102 3VILAGERENGERINETISTITTIEFS 111:	Query Match 53.7%; Score 520; DB 2; Longth 192; Best Local Similarity 65.6%; Pred. No. 5.6e-43; Matches 191; Conservative 27; Mismatches 24; Ender: 2; Gaps 2; Oy 2 POPIESKISVIRMINIQUESTICONESTEEMINISTICUMARISTIC INTO 1111; 1111 Oy 11:1	Nature 478, ***-41 1495 A;Tith-: Cloning of a new cytchine that induces IEN-gamma production by I cells. A, Peferrors number, 860226 A;Accession: 850226 A;Status: preliminary A;Molecule type: mRNA A;Posiducs: 1-192 <6KA A;Cross-references: EMHI-:049949: NID-glor4822: PID:dicovile: FID:dic64923	RESULT 1 S60426 Cytokine IGIF - mouse Cytokine IGIF - mouse C:Species: Mus musculus (house mouse) C:Date: 10-Apr-1946 #sequence_revision 19-Apr-1946 #text_change 10-Sep-1997 C:Accession: S60226 R:Okamura, H - Tsutsui, H - Komatsu T, Yutsude, M. Habura, A.: Tanimoto, T.: T
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G.Comment: C3a anaphysaccate is a vasoactive peptide and a addition of information.
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A:Title: Structure and expression of the C3 gene.
A:Reference number: I49563; MUID:84045280
A:Auccession: 149563
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fau, J.; Wardth, E.; submitted to GenBank, May 1998
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And N. Y. Acad Sci. 421, 207:212, 1983
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A: Description: Genome sequence of an obligate intracellulir pathorem of temans

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Protective (1) protein HF1508 - Hellocharter pylori (strain 26695)

CISPECIES, Hellocharter pylori

CISPECIES, Hellocharter pylori

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CiAccession (164-093)

RITOMBO (15) White O - Kerlavage A R : Clayton, R.A : Sutton, G.G.: Fleischmann, F.D.

Peterson, S - Leftus, P : Firhardson, D : Fudson, P.: Khilak, H G.: Slodek, A : McKonne

son, J.D.: Kelley, J.M.: Cotton, M.D.: Weldman, J.M.: Fujii, C.: Bowman, C.: Watthey, L
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A.Experimental source: serotype D. Strain UW-3/Cx
C/Genetics:
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A; Rosidues: 1-866 KARNS
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A_Title Clear
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C,Accession. A45532, A45531
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From Natl Arad Sel U.S.A. 65, St. 635, 1988
A.Title: The 3' partise of the Jose for a Plasmodian yealth corrective surface antigen
A.Peforence number: A28121; MOID:88124889
Arageession: A28121
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A.Experimental source. Strain 17XL
A.Noto the a thirs translated the older TTA for residue 417
T.Keywords. surface untigen
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A.A.D. 13 Hajes, M.S., Berldersky, M., Karpk, P.D.: Smith, B.O., Prason, C.M.: Vente A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylons.
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A:Residues: 1-175/L;177-192 <WIL>
A:Cross-references: EMBL:x55982; NID:q49714: PID:q49715
C:Superiamily: 01190(A) synthetase
C:Keywords: nucleotidyltransferase
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A:Intle: The murine 2 5A synthetase locals three distinct transcripts inches A:Reference number: S15660 MITD-01232952
A:Accession: S15661...
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A;Title: Nucleotide sequence of porcine interloukin-1 dipha
A;Reference number: 146620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrota prointerleukin-1 alpha mENA, complete cds - piq
C:Species- Sus scrota dumestica (domestic pig)
C:Cate- 21-Feb-1997 #Sequenc_revision 21-Feb-1997 #Fevt_-4-min
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C:Date: 31-Dec-1993 #seguence_revision n2-lun-1994 #roxt [chargo la-Sop-late C:Accession: S15661; S19108
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A.Status. preliminary, translated from GB/FWPL/NNBJ
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A; Residues: 1-192 <RUT>
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Best Local Similarity
183 TURISETRIEVSAQNEDERVILKELPETRKTIKDETSILLEFWEK----HONMOVEKSAAH
                                                                                                             11 KYMEMEVINHIIK NUAFMIEITEERSINTMAAVUMLUDDAVELUMAA IESULEÇUPV 18
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                                                                                                                                                                                                                                                              Y Match 9.3%; Score 75.5, DI Local Similarity 20.6%; Pred. No. 3.8;
                                                            63 TISVKCEKI-STLSCENKITSEKEM NPPDNIKDTKSDITFFCFSVP HHVKMCTESSSY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * KLSVIENINNĄVIETDĄYNEKIEEDMED····SDZETNAPETI EIISXIKDSCEGMAV 62
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121 EGYPLACEKER 121

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A.Molecule type: mRNA
A.Residues: 30-467 <A02>
                                                        RiBobertson, K.: Mason, I.
Submitted to the EMPT Distribution to the object embryo suggests roles in regionalisation
ArDescription Engression of out in the objects embryo suggests roles in regionalisation
                                                                                                                                                                                                                   ret protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-oct-1995 #sequence_revision 03-Nov-1995 #text_change 19-Dec-1997
C:Accession: $57450
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C:Superfamily protein kinase homology
C:Keywords: alternative initiators: prote-oboogene
E:136-388/lummain: protein kinase homology <KIN>
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A; Accession: S31639
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A.Reference number. A48713; MUID:94043034
A.Reference number. A48713
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J. Biol Chem 200, 22723-22732, 1993
A:Title: The human out proformongene encodes two protein scring/thronsing k
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A: Pesidnes: 1-467 /CHA
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A:Molecule type: mBNA
A:Pesidies 1:45 Arm
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CiSpectos: Mycoplasma genitalium
C.Dato 10:Nov-1245 #Sequence_recusion 10:Nov-1285 #ICAC_CHAD 12:Sep.1398
C.Accession. #64245
R.Frascr, C.M.: Socayne, ".D.; White, O.; Adams, M.D.; Clayton, B.A.; Eleison, M.; Fuhrmann, J.; Nguyen, D.; Citerteck, T.F.; Sawlek, D.M. Phillips, C.A.
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R:Ohara, R.: Miyoshi, J.; Aoki, M.; Toyoshima, K.
Rychara, R.: Miyoshi, J.; Aoki, M.; Toyoshima, K.
Dph. J. Cancer Res. 84, 518-525, 1993
Dph. J. Cancer Res. 84, 518-525, 1993
A;Title: The murrine and proto-cocogene : genome structure and tissue-specific express
A;Reference number: 149609; MUID:93308016
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A:Molecule type: mRNA
A:Freshjucs: 1:364 (FOB)
A:Cross-references EMBI 749898,
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A;Molecule type. mRNA
A;Rosidues. 1:467 <RES>
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C:Superfamily: protein-tyrosine kinase ret; protein kinase homology C:Keywords: AIP
E:714-1004/Pomain: protein Finaso homology <KIN-
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               ocayne. T.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. Nguyeu, D.; Otterhaek, T.B.; Sawleł, D.M. Phillips, C.A.; Merrick
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15-JUL-1998 (REL 36, CREATED)

15-JUL-1998 (REL 36, LASI SEQUENCE UPDATE)

15-JUL-1998 (REL 36, LASI ANNOTATION UPDATE)

17-TOTAL THE PEOPLE OF (IL-18) (INTERFERENT SAMMA INTUING FACTOR)

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SUBMITTED (FEB-1997) TO EMEL/CENBANK/DEBU DATA BANKS.
--- FUNDIAL NATURANS ANTIGHAL WILLER DELL ACTIVITY IN SPIEREN CELLS
AND STIMULATES INTERFERON GAMMA PROTUCTION IN I HELFER THEE I
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MEDITINE: 95247646.
MISHIO S., NAMBA M., OKUPA T., HATTOPI K., NUKADA Y., ATTANARE F., KONISHI K., MICALLEF M., FUJII M., TORISOE FUKUDA S., IKEDA M., OKAMUPA H., KURIMOTO M.:
J. IMMUNOL. 156:4274-4279(1996).
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MUSCULUS
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TIN. NYESI 79:469-474(19:47).

FUNCT: N. ATHERIS NATURAL KILLER CELL ÄTTIVITY IN SPLEEN CELLS
AND STEPLATES INTERFEREN SAMMA FROMETION IN THELPER TYPE I
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Cathy 65.6%; Pred. No. 66-4
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Bost Local
P18430;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
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Ouery Match 63.7%; Score 519 5; DB 1-
Best Local Similarity 65.9%; Fred. No. 6.7e-42;
Matches 93. Conservative 29; Mismatches 27;
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0.19073;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTERLEWIN-18 PROTUPESOP (IT-18) (INTERLEWIN-1 GAMMA) (IT JAMMA)
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THWAY: PHAMPH ALIEKNAIE PAIHWAY; PLASMA;
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A. STILBISIA, PETAT TOBIÇIRBD)
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                                                                   CRG FRAGMENT.
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THE FRAGMENT.
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COMPLEMENT C3, BETA CHAIN.
COMPLEMENT C3, ALPHA CHAIN.
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Matches 26,
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EMBL: J04668: G160493: -.
FIR: A28121: A28121.
PIR: A45532: A45532.
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PROC NATE ACAD SCI II S A 85-602-605(1988).

-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A 3PT-ANCHOR
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDIINE: 90205979. LEWIS A.P.:
                       CARBOHYD
                                  CARBOHYD
                                              CHAIN
                                                         SIGNAL
                                                                    MALARIA; MEROZOITE; POLYPROTEIN; REPEAT; SIGNAL: SLYCTEDIEIN TRANSMEMBRANE; GPITANCHOR.
                                                                                                                                                                                                                         STRAIN=17XL;
MEDLINE; 88124889
                                                                                                                                                                                                                                                                                                                                 PLASMODIUM BERGHEI YOELII.
EUKAKYSIA, PROTOZGA, APIN'MPIEXA,
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                                                                                                                                      FIM: MEROZÓTIE SUFFACE ANTIGEN CONTAIN THE SEQUENCE OF SOME KD AND 19 KD ANTIGENS WHICH ARE THE MAJOR SCHEACE ANTIGENS MEROZOTTES. THE MATURATION TAKE PLACE LURING SCHEZONT.
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MEDLINE, 9378616.

CHARA R. MINCSHI J., ACKI M., TOYOSHTMA K.,

JIN. J. CANCER RES. 84.518.525(1993).

-1. FUNCTION PROBABLE FOLE IN SIGNAL TRANSPOCITION.

-1. SUBCLIFICATE LOCATION ONTOFIASMIC.

-1. TISSUE SPECIFICITY HIGH IN ADDICT SUBMANDIBULAR GIAND, THYMUS,

SULDEN AND NEWBORN RIGHTSTYPE TEACT

-1. SIMILABILY WITH THE CONSERVED CATALIYIN CHMAINS OF SERVING-

-1. SIMILABILY WITH THE CONSERVED CATALIYIN CHMAINS OF SERVING.
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01-FEB-1995 (FEL 3) LAST SEQUENCE UPDATE)

01-FEB-1995 (FEL 3) LAST ANNUTATION TREATE)

207 FEGT TOWNSTARM SERIME/THEPTONIME FFF-LEIN KINASE (FC 2)
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UTF: PS0011: PPOTEIN_KINASE_DOM: 1
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PROSITE: PS01186: EGE_2: 1.
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LETT. OHEM. 270.1254(-18051(1995)).

FRICT. OHEM. 270.1254(-18051(1995)).

V.VA. MAY SLAY A BOLE IN THE STORAGE AND STABILIZATION OF FACTOR
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(REL. 36, LAST ANNOTATION OPDATE)
(BEL. 36, LAST ANNOTATION OPDATE)
CELL MULTIMERIN PRECURSOR.
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14 NUNEQVIETE GENERLEED - MIESECRENAPHIFIISMYKLSCHE MAVETSVECEE - 71

71 - ISTESCENKIISEKEMNEPDNIKOTKSDIIFEGKSVEGHDNKMOFESSSSYTSIYFELACEK 120

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Matches Query Match Best Local

/ Match 4.18, Local Similarity 21 9%:

Conservative

32; Mismatches

Score 74.5; Pred No 20;

DB 1; 65;

Lengtl. 1036; Slopul

21.

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RESULT 12
Y414_MYCGE
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Best Local Similarity
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HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 695 715 POTENT!
COMPLICT 420 420 LEFT COMPLICT 420 AX: 25230 MW; E551
                                              SEQUENCE OF 52-146 FROM N.A.
STRAINAATCC 33580 / G-37;
MEDLINE; 94075280 ...
PETERSON S.N., HU P.-C., BOTT K.F., HUTCHISON C.A. ITT-
J. BACTERIOL. 175:7918-7930(1993).
1 SIMILAFITY SFIONE TO THE MEATT, MEATT , MEATT FAMILY
EMBL: U39727; G1046129; -..
EMBL: U39727; G1046129; -..
EMBL: U39727; G1046129; -..
EMBL: U39727; G1046129; -..
EMBL: W16972 G405988; -..
TIGR: MG414; -..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQ
01-NOV-1497 (REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. SIFAIN-AIDD 13530 , G p7: MEDLINE; 96026346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MG414.
MYCOPLASMA GENITALIUM.
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                                      TRANSMEM
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1036 AA: 123
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21.9%;
   1.73179 MW:
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 POTENTIAL:
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RESULT 14
IL1A_BOVIN
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AC PCRR1
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Best Local
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01-JUL-1942 (PEL 25,
01-JUL-1943 (PEL 25,
01-N.V-1946 (PEL 32,
CENTROMERIO PROTEIN E
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ILIA_BOVIN STANDARD:
PCRASI:
01-NOV-1948 (RHL 09, CREATED)
                                                                                                                                                                                               1026
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PROSITE: PS99967: KINESIN_MOTOR_DOMAIN2: 1.
MOTOR PRILIN: 9881 CIVISION: AIR-HINGING COLLEG COLL; MITOSIS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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-1. SUBGELUULAR LOGALIGN: ASSOCIATES WITH KINETOCHOPES DURING CONGRESSION, PELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, COANTICATIVETY DISCAPOED AT THE END OF THE CELL DIVISION SIMILABITY. BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECTENCE FROM N.A.
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COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
AIF (BY SIMILARITY)
MK. FALFFORT CHOSE.
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Pred. No. 68,
35, Mismutches
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Best Local
RCCT_HUMAN STANDARD.

P41279;
P41279;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                               _HUMAN
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SEQUENCE
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-1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO, EMUS OF THESE PROJEINS SERVE SOME AS YET UNDERLINED FUNCTION.
-1- THE LACK OF A SPECIFIC HYGHOPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OF IS SECRELED BY A MECHANISM EIFFERING FROM THAT USED FOR OTHER
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EMBL: M36192: G163227: -.

EMBL: X12497: G445: -.

EMBL: M37210: G163199: -.
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MAL. IMMUM. 25.42.4.4.7(1488).
-!- PUNCTION: PRODUCED BY ACTIVATED MACPOPHAGES, IL-1 STIMULATES
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N. AFLYMAN I., MIYOSHI J., TOYOSHIMA K.:

N. ARL 6. LANG SELV(1991).

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WOOD V: RAJANDREAM M.A., BARBELL B.G., SKELTGN J.,
SUBMITTED (MAR-1997) TO EMRI/GENRANK/DUBJ DAIN HANKS
EMBL; ALCCCCC; ELCE6446; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                         MEDILINE: 97098008.

BOURKE P.F., HOLT F.F., SHIHEPLANDER J., KEMP K.J.:

"Discuption of a novel open reading frame of Plasmodium (alciparum chromosome 9 by subtelomeric and internal deletions onn load to lose on maintenance of cyteadherence.";

of maintenance of cyteadherence.";

MOI PROCESS NARASITOL 82:25-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLEEL 01, CREATED)
01-NOV-1996 (TREMBLEEL 00, LAST SEQUENCE UPDAIE)
01-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPTATE)
NOVEL OFF ON OHROMOSOME 9 (FRAGMENT).
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKAFYOTA: FUNTI: ASSUMYDSTA: ABUHIASSUMYDSTES:
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01-JUN-1998 (TREMBERE) 06, LAST SECUENCE UPDATE)
01-JUN-1998 (IREMBERE), 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 44.2 KD PROTEIN.
                                                                                                                                                                                                                                                                         PLASMODIUM FALCIPARUM.
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                                192 FLOEYNKKPEEDVONPGLLNNEKSDIYEIGIY------
111 NKMQFESSYEGYFLACEKERDLFKLILKKEDELGD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 ---- VSSKHLDYNSENYNKEDEDEDRT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EGYFCACEKERDLFKLILKKEDELGDRS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 - LFVKPLESNSALNSQNEHTEVQKKSNSIDNL - TPSSELFRKRS - - - RDNNLSRESS - -
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                                                                                                                                             21 FIRMONRPLEEDMIDSFORDNAPFITTISMYEDSOFROMAN 11 VENILE 1 1 SILLE 1 H
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                                                                                                                                                                               h 10.0%; Score 81.5; D
Similarit; 22.4%; Pred. No. 13;
35; Conservative 23; Mismatches
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084500;
01-NOV-1998
01-NOV-1998
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01-NOV-1906 (IHEMHIBHI 01 CREATED)
01-NOV-1908 (IHEMHIBHI 01 CASI SEQUENCE UPCATE)
01-NOV-1908 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
01-NOV-1908 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
0ATION-INCEPENCENT MANNOSCIS-FROSTHATE PROFESSES,
0ALLUS 3ALLUS (CHICKEN)
0ALLUS METACIA: THURDAIA VERTERBATA; ARTHOSAUP
ZHOU M., MA Z., SLY W.S.;
"Cluding and expression of the obna of chicken maticomindependent mannose 6 phosphate receptor.";
PROC. NAT. ACAE SCI. U.S.A. 32 9762-9766(1995).
EMBL. U35037; G1019119; -.
PEAM: PE00040; fn2; 1.
PEAM: PE000878; CIME repeat; 13.
SECULIAGE 3471.AA. 276645 MW. GRBGRE76 CE332.
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EMBL: AEO01322: G7328929; -.
SEQUENCE: 856 AA; 96583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MAPATHE R., ARAVIND L., MITCHELL W.P., OLIMSER L., TATUSOV R.L., ZHAO Q., KOONIN E.V., DAVIS R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome Sequence of an Obligate Intracellular Pathogon of Humans: Chlamydia trachomatis " . 
 SCIENCE\ 0:0-0(1998) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITCHELL W P
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BACTERIA: CHLAMYDIALES; CHLAMYDIACEAE;
                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDIINE GARAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-L/UW-3/CX:
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bes 34. Transposition 2
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METASTA: THUSHATA- VERTEBRATA; ARTHUSAUPIA. AVES
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TATUSOV
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Pred. No. 23;
CC Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBEREL 95, CREATED)
01-JAN-1998 (TREMBEREL 95, LASI SECTENCE OFDATE)
01-JAN-1998 (TREMBEREL 95, LASI ANNOTATION GENAT
HYPOTHETICAL 52.7 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AE000565; G2313624; -. TIGR: HP0508; -.
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AN-100 (CEEMBLREL 205, CAST SECRENCE OPERIE)
NOV-100 (CEEMBLREL 208, LAST ANNOTATION OPDATE)
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TONNELL M. CODSEY T. COOPER J. COULSON A., CRAXTON M.,
TONNELL M. CODSEY T. COOPER J. COULSON A., CRAXTON M.,
HILLER J. THER M. TOHNSTON L. JONES M., KERSHAW J.,
TALLER M. TALRETTLE F. LICHTNINT T. TICYD C.,
MICHAEL M. TALRACHAM M. FARSONS J. PERCY C.,
MICHAEL M. TATHERS D. FICWINGEN F. SMALDON N., SMITH A.
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THE SAME CONTROL MAY TO BANK TA CROSS.
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no as nucleatide sequence from chromosome III of C.
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21.08; Pred. No. 19;
10.09; 28; Mismatches 57; Indels
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Best Local Similarity 22.39
Matches 29; Conservative
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01-NOV-1996 (TEMPEREE, 01. LAST SEQUENCE UPDATE)
01-NOV-1998 (TEMPEREE, 08. LAST ANNOTATION UPDATE)
0NI ORF (FRAGMENT).
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
EUVARY TA METATIA, CHISTONIA VERTESHATA, ARCHASAUKIA, AVEST
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"Molecular cloning of equine interleukin-1 alpha and -beta cumas.":
vel. immunut immunutvafict. 48:221-231(1995).
EMBL: D42146: G1197798; -.
PROSTITE: PSO0253. INTERLEUKIN-1; 1.
PFAM; PF00340: Interleukin-1; 1.
SEQUENCE 270 AA: ved06 MW: 11246092 CEC32:
Übbübbd
                                                             06606d
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NON_TEK 1251 1251
SEQUENCE 1251 AA; 1
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MECH. DEV. 43:159-173(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 758 QUKQALELULGQAKKERDLAKVQITSIS--SEKSYBEKIMEE 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 -- SSSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVONE 156
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                                                             PRELIMINARY
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22.3%; Pred. No. 10;
ative 29; Mismatches 6);
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01-MAY-1997 (TREMBLREL, 03, CREATED) 01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)

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REGIONAL DESCRIPTION OF THE STREET OF THE ST
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01-NOV-1998 (TREMBLREL

01-NOV-1998 (TREMBLREL

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FAEL3 12 PROTEIN

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HENKHAUS J., WOHLDMANN P.:
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
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BURDTON TOWNERS M. CONSER T. COMPRED J. CONTISON A., CPANTON M.,
ETAR S. T. T. TICHPIN F. FAVETICA, FULLON L., SARDNER A., CREEN P
HAWKING T. HILLEF L. TIFF M. JOHNSTON L., TONES M., KEPSHAW J.,
KIRSTEN J. LAISSER N. LAIRBILLE P., LIGHTHING J., LLOYD C.,
MCRUTERAY A. MOSTIMORE P. COCALIAGHAN M., PARSONS J. PERCY C.
MCRUTERAY A. MOSTIMORE P. COCALIAGHAN M., PARSONS J. PERCY C.
PITKEN L. POOPPA A. SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A
SONNHAMMER E., STAGEN P. SULTON J. THIERPY-MIEG J. THOMAS K.,
VAUGHAN K., WATEPSTON P., WATSON A., WEINSTOCK L.,
WILKINSON-SPROAT J. WOHLDMAN F.,
WILKINSON-SPROAT J. WOHLDMAN F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WATERSTON R.:
STEMULTIPD (TENTIALE) IN EMBLING
EMBL: 080836: SITO7142: ".
PEAM: PERMOSU AFORMOS! I
SEQUENCE IOT AND (PICT KM
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EHKARYOTA: METAGGA: NEMATODA: SECERNENTEA: RHARDITIA: RHARDITIDA;
EHABDITINA: PHAFCITGIEA: PHAFCITHAE: FELGCEFINAE: CAENGRIARGITIS
                   APABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIPIDIPLANTAE: CHAROPHYTA/EMBPYOPHYTA GROUP; EMBRYOPHYTA:
TRACHEOPHYTA: FUERLI-OPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA;
EURICOTYLEDWINS: FOSIDAD CAPEARALES RPASSTOACFAE; AFABIDOPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
SIMILARITY TO A C3HC4-CLASS ZINC FINGER
B0432.9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------MAVTISVKOEKISTLSCENKIISFKEMNEPENIKOTKSOTT---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **SELEKONOKISATVOGHTYHHGOISQWIATKEQOPSGERTVPKNGEVEKLEFDVQENGGE 255
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08. LAST SEQUENCE UI
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                                                                                                                                                                                                                                         UPDATE)
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Prest Local &
Matches 34
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Matches 36; Conservative
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01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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127A16.28 FROTEIN.
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SOMBPVILLE O.B., VRNTER J.C.;
"AYABIJORGAS 153,150.5 CHILT SOME II BAC EGEI3 BESINI FOR SUBMITTER (JUN-1996) TO EMBL/GENEANK/JUBJ DATA BANKS.
EMBL: ACCUMUNS: G32/12856; ".
Q14275
Q14275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANIEY S.D., LIN X. KAUL S., SHEA T.F., FUGIL D.Y., MAGON T.M., FOUNTEY S.D., LIN X. KAUL S., SHEA T.F., FUGIL D.Y., MAGON T.M., SHEN M. FOUNTING O'M, FRANCE O'M, SUMERVILLE D.R., VENIER J.C.: "Arabidogsis thallar o'hteresien II BAC TOTALE Jendeli suljeddel": SUMMITTER (SEP-1998) TO EMEL-GENEANK/DDEJ DATA BANKS.

EMBL. ACUSAS-1998 TO EMEL-GENEANK/DDEJ DATA BANKS.

EMBL. ACUSAS-1998 TO EMEL-GENEANK/DDEJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKAPYCIA: VIPIDIFLANTAE, CHAPCTHYIA/EMBRYCFHYTA GECCT: EMERYC
IBACHE HHYIA, EUHHVIA/FHYTES, SFERMAIGEHYIA, MAGNILLZESYTA:
FUDIOCTYLECOMS, EUSILAE, OMFRASALES, BRASSICACEAE, ARMEICCTSIS
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                                                                                                                                                                                                                                                                                            SYEGYFLACEKERDLFKLILK-KEDE 143
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                                  PRELIMINARY;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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78, Pred. No. 48;
29; Mismatches 59, Indele
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Pred. No. 39;
                                  PRT:
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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EMBL: X66433; G509274; -;
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 CLOSTRIDIUM BOTULINUM.
BACIERIA: FIRMICHIES: RACHIUMS/MIOSIFIFIUM GROUD: CLOSTRIDIACEAE:
 "Organization of the botulinum neurotoxin Cl game and its associated nen-toxic protein genes in Clostridium botulinum C 468."; MENT 143-641-640(1994).
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PARASITOLOGY 113:439-448(1996).

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 BUMSTEAD J.M., DUNN P.P.J., TOMLEY "Nitrocollulose immunoblotting for
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 008759; P97482;
 SEQUENCE
 HYPOTHETICAL PROTEIN.
 NATURE 390:580-586(1997).
EMBL: AE091182: GZKR8785; -.
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SPOUENCE PROM N.A.
 BOPPELIA RUPGDORFERI (LYMF DISEASE SPIROCHETE)
BACTERIA: SPIROCHAETALES; SPIROCHAETACEAE; BOF
 051778;
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 134 PELFIATKED 143
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 Score 78; DB 9; Length 1146; pred. No. 90; 38; Mismatches 71; 1::dols 44;
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MUS MUSCULJS (MOUSE). EUKARYUTA: METAZUA, CHOEDATA, VERTEBRATA, MAMMALIA, DUTHERIA, RUUEHITA: SCIUROGNATHI: MURIDAE: MURINAE; MUS.

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 J. BIOL.
 HATTAKEYAMA S. JENSEN J.P., WFISSMAN A.M.:
"Subcellular localization and ubiquitin-conjugating enzyme (E2)
in-teractions of mammalian HECT family ubiquitin protein ligases.";
J. BIOL. CHEM. 272-15085-15092(1997).
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MEDLINE, 97316
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 14 MINEOVIEVONEOPVEE--PMTDIFOSASEEQTPLITYMYKESEVEGLAVTLSVKESKMS 71
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(ب)
 FUNCTION: INTERACTS WITH THE 66 PROTEIN OF THE CANCER-ASSOCIATED HUMAN PAPILLOMAVIKUS IYPES 16 AND 18. THE E6/66 AP COMPLEX BINDS TO AND TAPGETS THE FT THMMP SUFFEESORP PROTEIN FOR URIQUITIN MEDIATED PROTECLYSIS 66-AP IS AN E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN HEMM AN E2 UBIQUITIN-CONJUGATING ENZYME I THE FORM OF A INTESTEE AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TAPGETED SUBSTRATES.

SUBCELLULAR INCATION: NUMBER AND CYTOPLASMIC AND THYMUS. ISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS. ISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS. A CYSTEINE PESIDME IS REQUIPED FOR UBIQUITIN-PROTEIN LIGASE SIMILARITY. CONTAINS AN HEAT-TYPE E3 UBIQUITIN-PROTEIN LIGASE SIMILARITY. CONTAINS AN HEAT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
 CAUTION: IT IS UNCEPTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR
 . TRC1105 31847575;
MGI:105098; UBE3A.
(PECO632 HECT; 1
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 E6-Ap ubiquitin-protein ligase (PBB3A) gene is localized within owed Angelman syndrome critical region.";
ME pes 7:368-377(1997).
 WEINEE ---- FOREFIFESSECTIONS OF FRAK----- KGPRVDFLETELGVK-----
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NV -> KE (IN PEF. 2).
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LIPOXYGENASE.
 "Nucleotide sequence and spatiotemporal expression cholerae vieSAB genes during infection.";
J. BACTEPIOL 180-2230-2305(1998)
EMBL, AF031552; G3123890; -.
SENTENCE 1145 AA. 120484 MW TREEDIOL 7-1
 SUBMITTED (NOV-1997) TO EMBL/GENEANK/DEBJ |
EMBL; Y15410; E1172502; -
PROSTTE; PSOOR1; LIPOXYGENASE_1; 1.
PROSTTE; PSOO711; LIPOXYGENASE_1; 1.
PFAM; PFUUJUS; LIPOXYGENASE; 1.
SEQUENCE 866 AA; 97748 MW. GETOFSIS GE
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PISUM SATIVUM (GARDEN PEA).

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FRIMATUS; TALABETINE HUMINITAE; HOMO.
 "Largo Scale Segretor Analysis and Annotation with the Sequence computison Analysis (SCAN) System.":
SUBMITTED SET 1-0) TO FMHI JEFNHANK-PORT DATA BANKS.

FROED TAKE "ANTON: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

MRS. ACO: 1: 1840164
 SELTENCE IT SENT STRICK THENGUL, CONNOLLY K.S., GUNNING K.M., KANNES K., SCHER T., MILLER C., PITLOCK S., POLLARD M., ROJESKI H., STERRAMANIAS II., MARIIN C.H.:
 THE SCHEET OF TWO PROTEIN: THANSMEMBRANE: CALCIUM-BINDING: REPEAT SELVENCE OF AN OFFICE HOW REPEAT SELVENCE OF AN OFFICE HOW. (D921-03 CRC32)
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## SUMMARIES

Result

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| 4 از            | œ                |            | ٠.                 | ٠.           | 1 L                 | Ti State of Col                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| Lucry Match<br>Best Corol Similarity 18 09, Field Mr. 4.1; | A64070  A64070  A64070  Condepoptidase La (EC 3.4.21.53) - Haemophilus influenzae (strain Pd FW20)  Coppeles: Haemophilus influenzae  Coupeles: Haemophilus influenzae  Alaminae, To Coupele, M. 1995  Alaminae, M. 1995  Alaminae, To Coupele, M. 1995  Alaminae, M. | THE STATE OF THE S | Query Match  100.0%; Score 812; DP 2; Length 192;  Best Local Similarity 100.0%; Prod. No. 5 9e-58;  Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 NEGRIHOTIAVIENINE QUIEVLE REQUERE MILITER SASE POINT INTERVISE VEGIA 50  1 NEGRIHOTIAVIENINE QUIEVLE REQUERE MILITER SASE POTENTIAVIENI SEVENIA 95  16 NEGRIHOTIAVIENINE QUIEVLE REQUERE MILITER SASE POTENTIAVIENI SEVENIA 95 | S60226 C Species Mas museming (house mouse) C Species Mature 1996 #sequence_revision 19:Aprol996 #text_change 10:Sepci997 C Accession: S60226 Nature 378, 88-91, 1995 A:Title Cloning of a new mytokine that induces IEX-gamma production by T cells A:Accession: S60226 A:Accession: S60226 A:Status: proliminary A:Molecule type: mRNA A.Feridaes Traces |  | 40 71 8.7 2077 1 W22EE4 41 71 8.7 1494 2 C70152 sensory transducti 42 71 9.7 1381 2 S45781 probable calcium-b 43 70.5 8.7 1478 2 A71434 probable rank helic 45 70.5 8.7 1478 2 S73930 translation elonga |
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A:Molecule type: DNA
A:Residung: 283-576 /7005
A.ForsaireCriticus: EMBL.X91837, MID.dliT7517, EID.cul3814, FID.dli77549
A.Experimental source: strain EY1679
R:Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Evinori, submitted to the Protein Sequence Database, May 1996
 A:Molecule type: DNA
A:Posidings: [-499, N.,501-526 /HEA25
A:Posidings: [-499, N.,501-526 .NID.q171194, PID:q171195
A:Cross references, EMBL.M72716, NID.q171194, PID:q171145
E.Burtabil, I.: Coglingua, M.: Zaccaria, F.: Kilma, F.: Fiuschi. TV.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fradment from the left
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 A:Cross-references: SGD:S0003158; MIPS:YGL190c A:Map position: 7L
 A; Reference number: $64183
A; Accession: $64207
 A:Cross-references: EMB1:X41484: NIE-q114355: PID:c199121: PID:c1114355: R.Coq11evina. M. Deinerti D., Zaccaria. P.: Rima. F.: Bortani. I.: Brischi. T.V. submitted to the EMBL Data Library. September 1995
A:Description: A 6 7 Kb fragment from chromosome VII of Specharomyces convolvious cont
 A;Reference number: S31274
A;Accession: S31274
 A.Moto the authors translated the cuden TAT for revillat 116 as Val and OTT for resid
R:Healy, A.M.; Colubetowicz, S., Stapletob, A.E., Godbl. M., Sepubli Forch, A.A.; Pri
submitted to the EMEL Data Library, July 1991
 A:Gene: SGD:CDC55
 C; Genetics:
 A: Experimental source: strain S288C
 A; Molecule type: DNA
A, Residues: 1 526 KBRU/
 A;Reference number: S62051
A;Accession: S62055
 A; Molecule type: DNA
A; Residues: 1-281 <BER>
 ive new genes.
A. Reference number
 A)Cross references. EMBL.272712, NIC.41222810, PIC.4.43731, PIC.41222811, MIRS.VILLYO
 A; Accession: S61128
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Best Local Similarity 2011
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312 YLTVKIWDVNMDNKPLKTI-NIHE 334
 133 KLILKKKDENGDKSVMFTLTNLHQ 156
 268 L-CDNKTKTFEEYLDPINHN-----FFTEITSSISDIKFSPN---GPYIASED----
 217 CIPDOSENIVDIKETNMTELTEVITSAEHFGEGNLEMMSSSK: - CILKLODMBONS 250
 14 NINDQVI-FVDKRQPVFFDMTDIDQSASEPQTPITIYMYKDSFVPGLAVTLSVFDSEMST 72
 73 LSCKNKILSEEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACGKEDDAF 3/42
 3611128
 9.9%; Score 80.5; DB 2;
25.0%; Fred. NO. 4.7;
ative 29; Mismatches 56;
 Length 526
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RESULT 5

101467

Coxin, nontoxic component - Clostridium botulinum phase (type C)

1. Species - Tiestridium betulinum phage

2. Species - Tiestridium betulinum phage

3. Cross-references - EMBI - X62386; NTD-4558175; PID-440389

A. Accession - P0C237

A. Accession - P0C237
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botulioum hearitaxin associated protein ANTP-139 - Glostridium motulinum phage 10 (stra NAIHernate names: ANTP-139 protein C Species Clostridium botulinum phage 10 Apraciety strain C 469 C. Date: 19-Mar-1997 **eequence_revision OF-Jun-1997 **text_change 10.Sep-1997 C. Accession: S46400; S49106 C. Accession: S46400; S49106 C. Hauser J. F. Frond, M. W. Requet, F. Popoff, M.R. Mol. Gen. Genet 243: 631:640, 1994 A. Hittle: Grannization of the botulinum neurotoxin C1 gene and its associated non-toxic A. Accession: S46400 A. Accession: S46400 A. Molecule true. S46400 A.
 A.Wilecake Tigo TEST
A.Pesilles Tigo TEST
C.Comment: This nentoxic component is a constituent of 168(500K) toxin with two other
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 A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetical
A:Reference number: $38373
A:Accession: $38373
 Interleakia-1 beta precursor - pig
COSPecies Sus scrofa domestica (demestic pig)
COSPECT 20 May 1994 Escquence_Levision Ol-Lec-1995 #text_change 08-Sep-1997
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 A:Cross references. EMBL.X72793, RID:q516171, PID:q516174
A:Experimental source: strain 0 468
A:Experimental source: strain 0 468
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
 A:Molecule type: DNA
A:Residues: 1:1196 :
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A;Status: preliminary A:Molecule type: DNA
 R:Vandenbroeck, K., Eiten, P., Ber
Eur. J. Biochem 217, 45-52, 1995
 Query Match 9.9

Best Local Similarity 24.3

Matches 30, conservative
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 1078 LSLKNTDGINISSVKFKLINIDES 1101
 1070 ISTANTICINISEVAPATINITIES 1101
 1024 TSEEVIRNYESYLDNSYIRDSSKSLLEYNKNYQLYNYVEPETSLYE-----VNDNNKSY 1077
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A.Status: File.
A.Molecule type: DNA
A.Moslecule: 1-167 <BUL>
A.Pesidues: 1-167 <BUL>
A.Pesidues: 3E.TCTTLT: NIL.gl:91497
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C:Accession: A64401

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 A, Introns. 16, 2, 42, 5, 44, 1, C; Superfamily: interleukin-1
 hypothetical protein 31971—Thlumpila trade matis (overlyge I. Africa CW1/Iv)
CrSpecies: Chlamydia trachomatis
CrBate: 13:Sept1948 #sequence_revision 13:Sept1948 #rext_clange 13:Sept1948
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 A.Authors: Born-Jovsky, M.; Klack, H.F.; Fraser, C.M.; Smith, H.D.; Wiese, C.R.; Vento
A;Title: Complete genume sequence of the methanogenia arabaech, Methanogocous jannaso
A;Reference number: A64200: MUTD-96337999
 C:Species: Methanococcus jannaschii
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A, Molecule type. 1
A, Residues 1:106
 A;Reference number. A71460
A;Accession: D71461
 F;Stephens, F S.; Kalman, S
submitted to GenBank, May 1998
 C:Accession: D714
F:Stephens, F S.:
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 A; Map position. FOR733027-733530
 A; Accession: A64401
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 A; Fesidues: 1-267 - VAN-
 A:Status: preliminary
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 137 DMH 139
 153 NLH 155
 53 INTERPRESAVILINAM SERMETE SOKNE --- FILSKE SMOP --- PENTITUT STOLIFFOKEV 105
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 93 DIOSON TEFORFORMAMMETESSI MESHFILAGQKETGAFKI ILMFRGENGERSVMFTIT 150
 38 IIYNYKDATVEILANEDDBEDKELEKKYIERIEKKOKLIETEKIEEKRLNTYIEFPEGIS 97
 47 IIYMYKDSEVPGLAVTLSVKDSKM-----STLSCKNKIISFEEMDP------PENID 92
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 9.7%: Score 79; DB 2; Length 506
25.0%: Pred. No. 6.1;
 NIB.4200756, PID 9200753
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 Musmarches 40: Indels 31: Gaps
 DB 1: Length 270;
 55. Thobals 34.
 ----LHTPEHHK-FLFSSLK 150
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 Nature 390, 580-586, 19
A;Authers: Venter, J.C.
 kifrdser, C.M.: Casjons, S.: Huang, W.M.: Sutton, G.G.: Clayton, R.: Latsiara, R.: Son, D.: Peterson, J.: Kerlayage, A.R.: Quackenbush, J.: Salzberg, S.: Hauson, M.: Rewman, C.: Gardard, S.: Fajli, C.: Catton, M.D.: Horst: K.: Hoberts, K.: Hatch. Nature 390, 580-586, 1997
 hypothetical protein 880838 - Lyme disease spirochetc
0;Species: Rorrella burydorfeti (Lyme disease spirochete)
0;Pate: 13-Feb-1948 *sequence_revision 13-Feb-1998 **ext_change 05-Jun-1998
0;Accession: F70204
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Citato: $4.002, $4027, $30139; $57383

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 Yeast 11, 865-871, 1995
A.Title. Sequence and functional analysis of a 7.2 kl HNA transport containing
A:Reference number: $57353
 C;Genetics:
A;Map position: 2R
 A:Cross-references: EMBL:X71329
R;Rose, M.; Kiesau, P.; Proft, M.; Entian, K.D.
Yeast 11, 865-871, 1995
 A;Residues: 1-698 <ENT>
A;Cross-references: EMRI-24-025: NU-g538487; FID:45-0488, MIRSYMBETGO
B;Baur, A.: Schaaff-Gerstenschlaeger, I.: Boles, E.: Miosga, T.: Rose, I
 A)Cross references: EMBL:236025; WID:g536487; PID:g536488
A.Noto, the authoritie requeste was substitled to the EMBL tutu tillusty. September 199
 A; Molecule type: DNA
A; Residues: 1-698 < ROS>
 A:Molecule type: DNA
A:Residues: 1-369 <B
 A:Status: translation not shown
 A; Accession: S30139
 Yeast 9, 289-293, 1993
A;Title: Sequence of a 4.8 kb fragment of Saccharomyces recevising chromosome !!
 A; Molecule type: DNA
A; Residues: 1-698 <E
 A; Variety: strain S288C
 hypotherical protein YRF156. yeast (Sarcharomyons ouroelsdar)
N; Alternate names: hypothetical protein YBR1206
 A; Status: nucleic acid sequence not shown; translation not shown
 A:Reference number: $30136
 S46027
 Cucry Match

Output 19. Score 79.5: DB 2: Length 698:
Best Local Similarity 22.4%; Pred. No. 10;
Withher 30 Conservation 31 Migratches 43: Indels 37: Gaps
 Species: Saccharemyces cerevisiae
106 TRIPRNGLHNDKSI 119
 136 IK--KKDENGDKSV 147
 243 PELFLATKEQ 252
 119 ECHELACOKE 128
 76 KNKLISEEEMEPPENILG-IQSELIFEQKRVPJHNKMEFESSIVEGHFLAGGKELDAFKLI 135
 3 4 QRKPGSTBSITETTODTUNCTTDAHSEINQBCYESSEWLPNNVYMNTCKYEDKKME---- f **
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A.Status: preliminary; nucleic acid sequence not shown, translation not shown A.Molecule type: DNA
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